seq4-149-163-14.rpr

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Cidenties: Manage 18-Jun-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999 C; Accession: 148161  
R; Nakamura, T; Ushijima, T:; Ishizaka, Y:; Nagao, M.; Arai, M.; Yamazaki, Y:; Ishika Gene 140, 251-255, 1994  
A; Title: Cloning and activation of the Syrian hamster neu proto-oncogene. A; Reference number: 148161; MUID:94193007; PMID:7908275  
A; Residues: preliminary; translated from GB/EMBL/DDBJ  
A; Satus: preliminary; translated from GB/EMBL/DDBJ  
A; Residues: 1-1254 < RES  
A; Cass-references: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID:g747595  
C; Genetics: A; Gene: neu  
C; Superfamily: epidermal growth factor receptor; protein kinase homology C; Keywords: ATP  
F;718-983/Domain: protein kinase homology < KIN>  
F;726-734/Region: protein kinase ATP-binding motif
                                                                                                                                                                                              DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDF---NNFTV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -185 precursor - golden hamster
;Species: Mesocricetus auratus (golden hamster)
;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                           955 DVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPSSPMDSTFYRSLL
                                                                                                                                                                             EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE
                                                                                                                                                                                                                                       1076 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVA
                                                                                                                                                                                                                                                                                                   PLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGG
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                                                      ALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTI
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C; Superfamily: epidermal growth factor receptor; protein kinase homology C; Keywords: ATP; autophosphosphorylation; duplication; glycoprotein; phosphopprotein; phosphopprotein; phosphopprotein; phosphopprotein; signal sequence #status predicted <SIG.
F; 20-1260/Product: protein-tyrosine kinase neu #status predicted <NAT>
F; 58-680/Domain: transmembrane #status predicted <TWN>
F; 723-988/Domain: protein kinase homology <KIN>
F; 71, 739-988/Domain: protein kinase homology <KIN>
F; 71, 739-786gion: protein kinase ATP-binding motif
F; 71, 191, 263, 535-576, 634/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 758/Active site: Lys #status predicted
F; 758/Active site: phosphate (Tyr) (covalent) #status predicted
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86.6%; Pred. No. 4.8e-234;
ive 51; Mismatches 105; Indels
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Best Local Similarity 86.6#
Matches 1096; Conservative
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          PIDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVIYNIDIFESMPNPEGRYIF
                                                                                   THLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNC
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A; Accession: A00641
A; Molecule type: mRNA
A; Redestion: A00641
A; Molecule type: mRNA
A; Redestion: A00641
A; Redestion: A00641
A; Redestion: A00641
A; Redestion: A1210 - CULA
A; Cross-references: EMBL: X00588; NID: 931113; PIDN: CAA25240.1; PID: 9757924
A; Note: the authors translated the codon AAG for residue 540 as Asn
R; 18h1ii, S.; Xu, Y.; Stratton, R. H.; Ree, B. A.; Marlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A; Title: Characterization and sequence of the promoter region of the human epidermal A; Reference number: A25772; MUID: 85270438; PMID: 2991899
A; Recession: A25772; MUID: 85270438; PMID: 2991899
A; Accession: A25772
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-29 < ISH>
A; Residues: 1-20 < ISH
A; Residues: 1-20 <
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Atkreterence number: SJ0024

Atkreterence number: SJ0024

Atkreterence number: SJ0024

Atkreterence number: BMBL: X05370; NID: 931118; PIDN: CAA2966B.1; PID: 931119

R.Halley, J.D.; Waterfield, M.D.

Title: Contributory effects of de Novo transcription and premature transcript terming the contributory effects of de Novo transcription and premature transcript terming Affected them. 266, 1746-1753, 1991

A.TILE: CONTRIBUTORY effects of de Novo transcription and premature transcript terming Affected them. 266, 1746-1753, 1991

A.A.Roseidute type: DNA

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A.Roseidute
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                                                                                                                   A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant A;Reference number: A00641; MUID:84219729; PMID:6128312
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A;Molecule type: protein
A;Residues: 25-30,'S',32-51;454-467 <WEB>
rg, P.H.
Nature 309, 418-425, 1984
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epidermal growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (BC 2.7.1.112) erbB C;Species: Homo sapiens (man) C;Contains (man) C;Contains (man) C;Daceis: How-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999 C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143; R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.
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601 590 661 718

704

778

764 838 824 898 884

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C.Species: Mus musculus (house mouse)
C.Accession: A53183; A43818; S24942; A28841; A58325; I49643
R.Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.A.R. (A. M.C.) (A. M.C.) Phillips, H.K.; Qiu, T.H.; Copeland, M.G.; Earp, H.S.; Jenkins, N.A.A.R. (A. M.C.) 
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        PENRTDLHAFENLEIIRGRIKQHGQFSLAVVSLNITSLGLRSLKEISDGDVIISGNKNLC 470
                                                                                                                                                                                                                                                                                          CVARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRASPLTSIV
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                                                                                    FVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFL
                                                                                                                                       SAVVG---ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQM
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                                                                                                                                                                        A;Molecule type: protein
B;Mrcczkowski, B.; Mosig, G.; Cohen, S.
Nature 109, 270-273, 1984
A;Title: AFP-esimulated interaction between epidermal growth factor receptor and superco
A;Reference number: A38023; MUID: 84491554; PMID: 6325948
A;Areference number: A38023; MUID: Molecule kinases) can nick double-stranded DNA
A;Note: the EGF receptor activity
A;Note: the EGF receptor (and other tytosine kinases) can nick double-stranded DNA
A;Title: Punctional independence of the epidermal growth factor receptor from a domain rapidence: annotation; internalization signal growth factor receptor feeds to internalization of the EGF-receptor C;Generica: annotation; internalization signal
A;Content: Binding of EGF to the receptor leads to internalization of the EGF-receptor C;Generica: annotation; jobi.3-7pl.1
C;Generica: annotation; jobi.3-7pl.1
C;Generica: A;Generica: GDB:120610; OMIM:131550
A;Generica: Appl.3-7pl.3-7pl.1
C;Generica: Appl.3-7pl.3-7pl.1
C;Generica: Appl.3-7pl.3-7pl.1
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F)1047-1210/Region: inhibitory
F)1047-1210/Region: inhibitory
F)128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predid
F)745/Active site: Lys #status experimental
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                     J. Biol. Chem. 260, 5205-5208, 1985
A; Title: Identification of residues in the nucleotide binding site A; Reference number: A60143; MUID:85182650; PMID:2985580
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49.4%; Pred. No. 6.9e-122;
S.; Staros, J.V
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Qy 244 EQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVT 303 Db 234 NQCAAGCTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGRYSFGATCVK 293 Qy 304 ACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVT 363 Db 294 KCPRNYYVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRKVCNGIGIGEFKDTLSIN 352	OY 364 SANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEOLOVFETLEEITGYLYISAWPD 423	484 HTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRG		Db 652 IVGGLLFIVV-VALCIGLFWRRHIVRKRTLENGERELVEPLTPSGEAPNOAHLRILK 710 Qy 723 ETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPRANKEILDEAYVMAG 782	783	DD 833 EDRELVHKDLAARNOLVENHYKITTIN [1]	QY 963 KCWMIDSECRPRFRELVSEFSRMARDPQREVVIQ-NEDLGPASPLDSTFYRSLLEDDDMG 1021 Db	QY 1082 APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTC 1139 Db	1088 - PVPEYVNQ-SVPKRPAGS 1200 PEYL-TPQGGAAPQPHPPF 1136 PEYLNTAQP	Qy 1243 FKGTPTAENPEYLGLDVP 1260
R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B. Oncogene 6, 673-676, 1991 A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding sit A;Reference number: A43818; MUID:91232866; PMID:2030916 A;Recession: A43818 A;Molecule type: mRNA A;Residues: 1-714 <avi>A;Coss.references: GB:X59698</avi>	Rigibanger, D.P.; Servero, G. Rubmitted to the EMBL Data Library, June 1992 A; Reference number: \$24942 A; Reference number: \$24942 A; Rolecule type: mRNA A; Residues: 969-971, K', 973-1115, 'D' < EIS> A; Athersores: EMBL: \$215.00 B; Rieisermann, G.J.; Gill, G.N.	J. Biol. Chem. 263, 13152-13158, 1988 A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylated i A;Reference number: A28941; MUD:88330814; PMID:3138233 A;Accession: A28941 A;Molecule type: protein A;Residues: 689-694, X, 696-704, L', 706-707;989-992, XX', 995-996, X', 998-1000;1002-1009, R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.	Budbalton: The Embl. Data Library, April 1974 A; Reference number: S45325 A; Actering 1985 A; Section: Action 1985 A; Section 1985 A; Section 2085 A; Section	R; Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K. Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993 A; Title: Expression of the epidermal growth factor receptor gene is regulated in mouse by A; Reference number: 149643; MUID:93126380; PMID:7678348 A; Accession: 149643	A;Status: trainstated from ob/Embi, DDBJ Molecule type: mRNA A;Residues: 12-20, 22-132 <res> A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201 C;Genetics:</res>	A; Userfamily: epidermal growth factor receptor; protein kinase homology C; Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphopro C; Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphopro F; 1-2-4/Domain: signal sequence #status predicted <sig> F; 648-670/Domain: transmembrane #status predicted <tmm> F; 712-977/Domain: protein kinase homology <kin> F; 712-7: 8/Region: protein kinase ATPP-binding motif F; 680-695/Binding site: phosphate (Thr) (covalent) #status experimental</kin></tmm></sig>	ro 근 X	MACCHES 53; CORBETVALIVE 1/1; MISHBACCHES 538; INDELS 118; CAPS 23; QY	129 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDFNNFTVSFWLRVPKVSA STANKTGLRELPMRNLOGILIGANPOLCYQDTILWKDFNNFTVSFWLRVPKVSA STANKTGLRELPMRNLOGILIGAVRFSNNPILCNMDTIQWRDIVQNVFM	PLPTDCCH : RSPSDCCH

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epidermal growth factor receptor, HER4 - human
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A47253
R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.;
Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HER4/p180erbB4, a fourth member of the epiderm
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SINATNIDSFKNCTKINGDVSILPVAFLGDAFTKTLPLDPRKKLDVFRTVKEISGFLLIQA 416
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C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor receptor spredicted cSIG>
F;1-30/Domain: signal sequence #status predicted cSIG>
F;31-64/Domain: extracellular #status predicted cEE1>
F;31-64/Domain: EGF receptor extracellular domain repeat cEE1>
F;397-610/Domain: EGF receptor extracellular domain repeat cEE2>
F;58-122/Domain: itracellular #status predicted cINM>
F;739-75/Domain: intracellular #status predicted cINT>
F;739-84/Domain: intracellular #status predicted cINT>
F;739-84/Domain: protein kinase homology cKIN>
F;739-735/Region: protein kinase ATP-binding motif
F;739-735/Region: protein kinase ATP-binding site: carbohydrate (Thr) (covalent) #status predicted
F;182_650/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat
                                                        Pydermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: A00643
R;Lax, I: Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennstr Mol. Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: CDNA cloning, expression in mou A;Reference number: A27720; MUID:88261272; PMID:3260329
A;Rolecule type: MRNA
A;Residues: 1-1223 «LAX»
A;Residues: 1-1223 «LAX»
A;Residues: 1-1223 «LAX»
A;Residues: 1-1223 «LAX»
A;Residues: 1-123 «LAX»
A;Reference number: A00643; MUID:85228222; PMID:2988784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LIYLPTNASLSFLQDIQEVQGYVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 RWGLLLALLPPGAA----STOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
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45.4%; Score 3110.5; DB 1; Length 1223;
Best Local Similarity 48.5%; Pred. No. 1.1e-119;
Matches 632; Conservative 172; Mismatches 349; Indels 149; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A00643
A;Molecule type: mRNA
A;Residues: 585-1223 <NIL>
A;Cross-references: GB:M10066
C;Genetics:
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                                                                                                                                                                                                  Gaps
A;Reference number: A47253; MUID:99189574; PMID:8383326
A;Accession: A47253
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-1308 «PLO>
A;Cross-references: GB:LD7868; NID:9337359; PIDN:AAB59446.1; PID:9337360
A;Note: sequence extracted from NCB1 backbone (NCBIP:126842)
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
F;716-981/Domain: protein kinase homology «KIN»
F;724-732/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                  191;
                                                                                                                                                                      Length 1308
                                                                                                                                                                    / Match 43.4%; Score 2972.5; DB 2; Length Local Similarity 45.1%; Pred. No. 4.7e-114; hes 613; Conservative 185; Mismatches 369; Indels
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A;Reference number: S13807; MUID:91125882; PMID:1846957
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A;Map position: Y
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A;Introns: 872/2; 898/1; 947/1; 979/3; 1025/3; 1056/1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP, growth factor receptor; phosphotransferase; transmembrane protein;
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-1166/Product: kinase-related transforming protein (Tu) #status predicted <MAT>
F;707-972/Domain: protein kinase homology <KIN>
F;715-723/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish N;Alternate names: epidermal growth factor receptor homolog; kinase-related transf C;Species: Xiphophorus maculatus (southern platyfish)
C;Species: Xiphophorus maculatus (southern platyfish)
C;Accession: So6142; S13809
R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, A.; R. Nature 341, 415-431, 1989
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing A;Reference number: S06142; MUID:90015140; PMID:2797166
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                                                                                                                                                                    ERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNED-LGPA 1003
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:| | | ::|| ::|| --EIGHSPPPAYTPMSGNQFVYRDGGFAAEQGVSVPYRAPTSTIPBAPVAQGATAEIFDD
                                                                                                                                                                                                   EKLPQPPICTIDVYMVMVKCMMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLP
                                                                            ADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKG
                                                                                                  ADGGKMPIKWMALECIHYRKFTHOSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKG
                                                                                                                                                                                                                                                                       SPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGG
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A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 821-1025, N',1027-1098, A',1100-1166 <ADA>
A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
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A;Residues: 1-1166 <WIT>
A;Residues: 1-1166 <WIT>
A;Cross-references: EMBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291
B;Adam, D.; Maeueler, W.; Schartl, M.
Oncogene 6, 73-80, 1991
A;Title: Transcriptional activation of the melanoma inducing Xmrk oncoge
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Length 1166;

Score 2674; DB 1; Pred. No. 6.1e-102;

39.0%;

Query Match Best Local Similarity

Matches Matches A B & B & B & B & B & B & B & B & B & B	575; Conservative 165; Mismatches 385; Indels 152; Gaps 31;	4 AALCRWGLILALLPPGAASTQVCTGTDWKLRLPASPETHLDMLRHLYQGCQVVQGN 59	8 AALLQLLLVLSISRCCSTDPDRKVCQGTSNQMTMLDNHYLKMKKMYSGCNVVLEN 62	60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119	63 LEITYTQENODLSFLQSIQEVGGYVLIAMNEVSTIPLVNLRLIRGQNLYEGNFTLLVMSN 12	120 GDPLNNTTPVTGASPGGLRELOLRSITEILKGGVLIORNPOLCYQDTILWKDFNNF 175 123 YOK-NPSSPDVYOVGLKOLDISNITEILSGCVKYSHNPILCNNFFINWMNTVNFFSNP 179	6 TVSFWLRVPKVSASHLENRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCK 23	:: :	235 GPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGR 294		295 YTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGME 354	290 YTFGAACVKECPSNYVYTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPKVCDGIGIG 347	S HEREVRAVTSANIQEFACKKIFGSLAFLEBSFDGDPASNTAPLQPEQLQVFETLEBITG	8 SESNITAVNSINIKSFSNCIKINGDILLNKNSFEGDPHYKIGTMDPEHLMNLTTVKEITG 40	415 YLYISAWPDSLPDLSVFQNLQVIRGRILHNGAXS-LTLQGLGISWLGLRSLRELGSGLAL 473	I HHNTHLCFVHTVPWDOLFRNPHOALLHTANRPEDECVGEGLACHOLCARGHCWGBGPTO 5	: : : : :	534 CYNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVAC 593		594 AHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQR 653	580 AHFODGPQCIPRCPHGILGDGDTL-IWKYADKWGQCQPCHQNCTQGCSGPGLSGCRGD-I 637	654 ASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMP 713 	4 NQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEI 77	: : :	774 LDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCM 833	7	4 QIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEXHADGGKVPIK 	WMAI.PGTI.BDDEFTHOCONWCYCHWINET WHOCANDOCTER AND TAKE TO COLORS OF THE C		4 TIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRS 10	: ::	114 LLEDDDMGDLVDAEEYLVPQQGFFCPDFAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSE 1073	94
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C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C;Dates: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C;Accession: A356223; E59164
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epiderma
A;Reference number: A36223; MUID:90083234; PMID:2687875 A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: 1-1342 <RRA>
A;Cross-references: GB:M29366
B;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro,
Proc. Natl. Acad. Sci. U.S.A 87, 4905-4909, 1990
A;Title: Molecular cloning and expression of another epidermal growth factor receptor
A;Reference number: I59164; MUID:90311312; PMID:2164210 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Gonetics: GB:M34309; NID:g18390; PIDN:AA35979.1; PID:g306841
C;Gonetics: GB:EMBBJ; HERB
A;Gonetics: GB:M1980; OMIM:190151
A;Molecule type: MID:g13-12413
A;Molecule type: MID:g1809; OMIM:190151
A;Molecule type: MID:g1809; OMIM:190161
A;Molecule type: MID:g1809; OMIM:190161
A;Molecule type: MID:g1809; OMIM:1909; OMIM:1909; OMIM:1909; OMIM:1909; OMIM:1909; OMIM:1909; OMIM: 1132 1054 1179 1180 SPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAP 1239 32; 188 ASHLENRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGC-ARCKGPLPTDCCHEQC 246
113 EIVVKDNGRSCPPCHEVCKG-RCWGPGSEDCQTLTKTICAPQCNGHCFGPNPNQCCHDEC 231 68 NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT 127 128 PVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDFNNFTVSFWLRVPKVS 187 126 ----NSSHALRQLRLTQLTEILSGGVYIBKNDKLCHMDTIDWRDIVR------DRDA 172 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 306 10 GLLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT 67 11 GLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGH 70 1074 EEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDG 1133 YVAPLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTL ------PVRENSITLRNISDPTQNALEKDLDG kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human Query Match 35.3%; Score 2418.5; DB 2, Length 1342; Best Local Similarity 40.4%; Pred. No. 1.8e-91; Matches 532; Conservative 192; Mismatches 458; Indels 135; Gaps ----EPCI PPTGH----1240 PSTFKGTPTAENPEYLG 1256 1140 TGNGMFLPAAENLEYLG 1156 A; Accession: I59164 ઢ g ઠે g ઠે 8 ઠે а 셤 쉽 ò δ ò g δ g

Nylletructus promett taccour interpretor nomolog precursor - rat
Nylletructs names: ErbB3 protein; HER3 protein
C; Bactes Rattus norvegicus (Norway rat)
C; Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
C; Accession: JC4387
R; Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
R; Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
A; Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein
A; Reference number: JC4387; MUID:96096535; PMID:8522196
A; Accession: JC4387
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1.1339 <-HEL>
A; Molecule type: The authors translated the codon AAC for residue 369 as Thr and GTT for residue C; Comment: This protein is a functional heregulin receptor that transduces signals to C; Comment: This protein is a functional heregulin receptor that transduces signals to C; Comment: ErbB3
A; Gene: ErbB3
A; Gene: ErbB3
A; Gene: BrbB3
A; Gene: BrbB3 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane protein F;10-1339/Pomain: signal sequence #status predicted <SIG> F;20-1339/Product: epidermal growth factor homolog #status predicted <NMT> F;640-659/Domain: transmembrane #status predicted <TMM> F;713-721/Region: protein kinase homology <KIN> F;713-721/Region: protein kinase ATP-binding motif F;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosphate (Tyr) 179 165 60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119 236 296 416 221 382 YGGVCVASCPHNFV-VDQTFCVRACPPDKMEVD-KHGLKMCEPCGGLCPKACEGTGSG-- 337 417 YISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIH 475 398 NIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRVYIS 457 534 222 NPNQCCHDECAGGCSGPQDTDCFACRRFNDSGACVPRCPEPLYYNKLTFQLEPNPHTKYQ 281 297 FGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHL 356 338 SRYQTVDSSNIDGFVNCTKILGNLDFLITGLNVDPWHKIPALDPEKLNVFRTVREITGYL 397 517 594 577 HYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSC--VDLDDKGCPAEQ 652 59 62 LQVLC----FLLSLARGSEMGNSQAVCPGTLNGLSVTGDADNQYQTLYKLYEKCEVVMGN 3 LAALCRWGLLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 237 LPIDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDIFESMPNPEGRYT VNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACA 476 HNTHLCFVHTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQC ANQQLCYHHSLNWTRLLRGPSEERLDIKYDRPLGECLAEGKVCDPLCSSGGCWGPAPGQC WLRVPKVSASHL - - ENRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGC - ARCKGP 357 REVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYL Indels 165; Gaps 34.2%; Score 2341.5; DB 2; Length 1339; 40.5%; Pred. No. 2.4e-88; Best Local Similarity 40.5%; Pred. No. 2.4e-88; Matches 523; Conservative 174; Mismatches 429; 535 63 166 595 셤 ò 엄 ઠે 셤 ò 셤 ò a ò 요 ò 유 ò 셤 ઠે 셤 ઠે 셤 ò

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RESULT 10 JC4387 18;

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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Accession: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999 C;Accession: A00644; A38022 R;Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K. Cell 35, 71-78, 1983 A;Title: The erbB gene of avian erythroblastosis virus is a member of the src gene A;Reference number: A00644; MUID:84026539; PMID:6313229
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A;Residues: 1-604 <YAM>
A;Residues: 1-604 <YAM>
A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678
A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678
B;Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Science 224, 1456-1459, 1984
A;Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new A;Reference number: A38022; MUID:84223957; PMID:6328658
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                                                                                               125;
                                                 698;
                                                 Length
                                                                                            Indels
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                                                                  Best Local Similarity 52.24; Pred. No. 3.4e-65; Matches 374; Conservative 80; Mismatches 137;
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    #status predicted
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    7;229/Active site: Lys
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C. Species: avian leukosis virus, ALV.

C. Species: avian leukosis virus, ALV.

C. Spate: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999

C. Accession: B00643; A00643

R. Nilsen, T. W. Maroney, P. A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M. Cell 41, 719-726, 1985

A; Fitle: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and prodession: B00643; MUID:85228222; PMID:2988784

A; Reference number: A00643; MUID:85228222; PMID:2988784

A; Recession: B00643

A; Molecule type: mRNA

A; Residues: 1-698 «NLL.

A; Cross-references: GB:MIO066; GB:MI3881; NID:9211749; PIDN:AAA48763.1; PID:9211750

A; Note: in Genbank entry CHKERBBF, release 109.0, the source is designated as Gallus gal C; Comment: This protein is synthesized as a gag-env-erbB protein.

C; Genetics:

A; Gene: gag-env-erbB

C; Superfamily: epidermal growth factor receptor; protein kinase homology

C; Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific profession: protein (fragment) #status predicted <AGAG.

F; 0-6) Product: gag protein (fragment) #status predicted <AGAG.

F; 0-698 / Product: gag protein tyrosine kinase erbB #status predicted <AGAG.

F; 0-698 / Product: protein kinase homology kKINs.

F; 10-7-89 / Region: protein kinase ATP-binding motif
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                                                                         LMSKPHLVIAVTVG--LAVILMILGGSFLYWRGRRIQNKRAMRRYLERGESIEPLDPS-E
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HFRDGPHCVNSCPHGILG -- AKGPIYKYPDAQNECRPCHENCTQGCNGPELQDCLGQAEV
                                               RASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGA
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A, Reference number: 835743
A; Accession: 835745
A; Accession: 835745
A; Molecule type: DNA
A; Residues: 1-544 < v EN>
A; Cross-references: EMBL:X12707
A; Cross-references: EMBL:X12707
A; Cross-references: EMBL:X12707
A; Cross-references: EMBL:X12707
C; Genetics:
A; Genetics:
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Superfamily: protein kinase homology < KIN>
F; 135-400/Domain: protein kinase homology < KIN>
F; 143-151/Region: protein kinase APP-binding motif
F; 170/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermal growth factor receptor - fruit fly (Drosophila melanogaster)
N;Contains: protein-tyrosine kinase (BC 2.7.1.112) erbB
C;Species: Drosophila melanogaster
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999
C;Accession: A00640; A38021
R;Livrahch, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.
Call 40, 599-607 1985
A;Title: The Drosophila EGF receptor gene homolog: conservation of both hormone bindi A;Reference number: A00640; MUID:85124611; PMID:2982499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1117 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER
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                                                                                                                                                                                                                                                                                                                                                                       644 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
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                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                              Length 544;
                                                                                                                                                                                                                            Query Match
24.1%; Score 1647; DB 2; Length 5
Best Local Similarity 54.9%; Pred. No. 2e-60;
Matches 345; Conservative 70; Mismatches 121; Indels
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 A;Accession: A38022
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossidues: 1-28, W', 30-139, F',141-145, V',147-152 <DEB>
A;Cross-references: GB:K02006
C;Genetics: A;Gene: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
F;130-135/Donain: protein kinase homology <KIN>
F;130-135/Donain: protein kinase Arp-binding motif
F;136-146/Region: protein kinase Arp-binding motif
F;165/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                       118 APNOAHLRILKETEFKKVKVLGSGAFGTIYKGLMIPEGEKVKIPVAIKELREATSPKANK
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                                                                                                                                                                                                          24.9%; Score 1703; DB 1; Length 604;
52.2%; Pred. No. 1.1e-62;
iive 76; Mismatches 128; Indels 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1254
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Matches 360; Conservative
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                                                                                                            651 TDEEGRECFORHPEC---NG---CTGPGADDCKSCRNFKLFDANETGPYVNSTMFNCTSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                  959 MIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLG--PASPLDSTFYRSLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1074 EEAP-----RSPLAPSEGAGSDVFDG---DLGMGAAKGLQSLPTHDPSPLQRYSEDPTV
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                                                                                                                                                                            CPLEMRHVNYQYTAİGPY-----CAASPPRSSKITANLD-
                                                                               ---NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYK-
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A;Gene: FlyBase:Egfr
A;Gross-references: FlyBase:FBgn0003731
A;Gross-references: FlyBase:FBgn0003731
A;Gross-references: FlyBase:FBgn0003731
A;Gross-references: FlyBase:FBgn0003731
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphor
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphor
F;173-764/Domain: extracellular #status predicted <TMM>
F;765-1330/Domain: intracellular #status predicted <TMN>
F;868-1072/Domain: protein kinase homology <KIN>
F;868-1072/Domain: protein kinase ATP-binding motif
F;122,300,324,363,518,688,695,700/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;774/Binding site: Lys #status predicted
F;1181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict
                                                                                                               re
A;Accession: A00640
A;Molecule type: DNA
A;Resions dides: L1130
A;L1130
A;Resions EBD.
A;Cross-references: EMBL: K03054
B;Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.
Nature 314, 178-180, 1985
A;Title: A Drosophila genomic sequence with homology to human epidermal growth factor A;Reference number: A38021; MUID:85137938; PMID:2983232
                                                                                                                                        A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 'A',812-866,'V',868-943,'OTPSLVK' <WAD>
A;Cross-references: EMBL:X02293; NID:g7922; PIDN:CAA26157.1; PID:g929565
C;Comment: This sequence is tentative because the introns have not been identified.
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.0%; Score 1642.5; DB 1; Length 1330; 29.8%; Pred. No. 7.2e-60;
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Best Local Similarity
Matches 414; Conserv
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1117 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1175
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                                                                                                                                                                                                                                                                                                                                                                             1062 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1116
                                                               15;
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                                                                                                                                                                                                     ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR 822
                                                                                                                                                                                                                                                                    YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE 942
                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                         Gaps
C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Reywords: ATP; phosphortanaferase F;135-400/Domain: protein kinase homology <KIN>F;143-151/Region: protein kinase ATP-binding motif
                                                              92;
                                             Length 545;
                                           Query Match 23.9%; Score 1640; DB 2; Length 54 Best Local Similarity 54.9%; Pred. No. 3.8e-60; Matches 345; Conservative 69; Mismatches 122; Indels
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Search completed: July 22, 2003, 09:08:44 Job time : 32.0157 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

July 22, 2003, 08:12:49; Search time 10.2793 Seconds (without alignments) 5088.033 Million cell updates/sec Run on:

Title: Perfect score: 6 Sequence:

SEO4-149-163-14
6848

MELAALCRWGLLIALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892 segs, 41476328 residues Searched:

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P04626 homo sapien	4 rattu	<u>ر</u>	6	Q01279 mus musculu	Q15303 homo sapien	Q62956 rattus norv	P13388 xiphophorus		9 rattu	P04412 drosophila		P00535 avian ervth	3 avian	7 gallus	æ	P70424 mus musculu	002466 branchiosto	P14616 homo sapien	4	P06213 homo sapien	P14617 cavia porce	7	Q25410 lymnaea sta	-	Q25197 hydra atten	P08069 homo sapien	Q60751 mus musculu		'n	homo	4 gallu	38 drosoph
	QI	ERB2 HUMAN	ERB2_RAT	ERB2_MESAU	EGFR_HUMAN	EGFR MOUSE	ERB4_HUMAN	ERB4 RAT	XMRK XIPMA	ERB3 HUMAN	ERB3_RAT	EGFR_DROME	ERBB_ALV	ERBB AVIER	ERBB_AVIEU	EGFR_CHICK	LT23_CAEEL	ERB2_MOUSE	ILPR_BRALA	IRR_HUMAN	IRR_MOUSE	INSR_HUMAN	IRR_CAVPO	INSR_RAT	MIPR_LYMST	INSR_MOUSE	HTK7_HYDAT	IG1R HUMAN	IG1R_MOUSE	IG1R_RAT	INSR_AEDAE	EPB4_HUMAN	EPB1 CHICK	INSR_DROME
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* Ouerv	Match	98.0	86.5	86.4	46.2	45.9	٠	43.2	39.3	35.4	4.	B	25.5	4	c	n	σ	16.7	10.7		10.4	10.3	0	10.2	•	10.2	٠	٠	•	•	9.1			9.6
	Score	6019		5914.5	3162		2972.5	2959	2690.5	2427.5	2364.5		1749.5	1703	1630	1611	1302	1142.5	734	714	714		699.5	869		696.5	665	649		636.5	622		591.5	σ.
Result	No.	-	7	n	4	2	9	7	æ	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q03145 mus musculu P07949 homo sapien	P54761 mus musculu P29317 homo sapien	091571 xenopus lae	Q00944 gallus gall Q91736 xenopus lae	Q91738 xenopus lae P54762 homo sapien	P53356 hydra atten P34152 mus musculu
EPA2 MOUSE RET HIMAN	EPB4 MOUSE EPA2 HUMAN	EPBA_XENLA	FAK1_CHICK EPBB_XENLA	FAK1 XENLA EPB1 HUMAN	HT16_HYDAT FAK1_MOUSE
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589.5	585 584.5	577.5	573.5	569 568.5	567 563
3.4	36	38	4 4 0 1	4 4 2 8	4 4 4 0

ALIGNMENTS

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DISULFID
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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PUTENTIAL.
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
ATP (BY SIMILARITY).
BY SIMILARITY.
                    RESIDUES (BY SIMILARITY).
POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00261; FU; 3.
SMART; SM00219; TYRC; 1.
SMART; SM00219; TYRC; 1.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_TYR; 1.
PROSITE; PS0011; PROTEIN_KINASE_ON; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000494; EGFR L domain.
InterPro; IPR00019; Euk_pkinase.
InterPro; IPR00119; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00145; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
Pfam; PF00069; pkinase; I.
Pfam; PF001030; Recep_L_domain; 2.
Pfam; PF001030; Recep_L_domain; 2.
ProDom; PD00001; Euk_pkinase; 1.
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EMBL; M11761; AAA35808.1; JOINED.
EMBL; M11762; AAA35808.1; JOINED.
EMBL; M11763; AAA35808.1; JOINED.
EMBL; M11763; AAA35808.1; JOINED.
EMBL; M11766; AAA35808.1; JOINED.
EMBL; M11766; AAA35808.1; JOINED.
EMBL; M17766; AAA35808.1; --
EMBL; M17766; AAA35808.1; --
EMBL; M17766; AAA35808.1; --
EMBL; M1730; AAA75493.1; --
EMBL; M3363; CAA27060.1; --
PIR; A25491; A25491.
PIR; A25491; A25491.
HSSP: P11362; IFGK.
GENEW; HGNC: 3430; ERBB2.
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SIGNAL
CHAIN
EJGNAL
CHAIN
DOMAIN
TRANSMEM
655
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NP BIND
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                                                                                                                                          VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLE 1016
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     AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
                                                                                                          LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
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                                                                        KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA
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"The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                         01-JAN'1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 37, Last annotation update)
Receptor protein-tyrosine kinase erbs-2 precursor (EC 2.7.1.112)
(p188srbs2) (NEU protein kinase erbs-2) (Epidermal growth factor erceptor related protein)
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TISSUE-Neuroblastoma;
MEDLINE-86118662; PubMed=3945311;
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TISSUE-Sciatic nerve;
MEDLINE-91222560; PubMed-2025425;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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R InterPro; IPR000494; EGFR L domain.

R InterPro; IPR0001719; Euk pkinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR00169; VIP_motif.

R Pfam; PF00169; Pkinase.

R Pfam; PF001030; Recep_L domain; 2.

R Pfam; PF00105; Furin-like; 1.

R Pfam; PF00105; Furin-like; 1.

R Pfam; PF00105; Furin-like; 1.

R Pfam; PF00109; Pfortin KINASE ATP; 1.

R RNOSTIE; PS00107; PROTEIN KINASE TYR; 1.

R PROSTIE; PS00101; PROTEIN KINASE DOM; 1.
STRUCTURE BY NWR OF 650-668.

MEDLINE=92155181; PubMed=1346763;
Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey D.,
Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
"Three dimensional structure of the transmembrane region of the proto-
oncogenic and oncogenic forms of the neu protein.";
EMBO J. 11:43-48(1992).
                                                                                                                                                                                                                                                                                                   tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
SUBCNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                         -i- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN.

-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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PIR; A24562; TVRTNU.
HSSP; P11362; 1FGK.
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ISSUE=NEVEC;

MEDLINE=94193007; PubMed=7908275;

MEDLINE=94193007; PubMed=7908275;

Makamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M.,

A Yamazaki Y., Ishikawa T.;

"Cloning and activation of the Syrian hamster neu proto-oncogene.";

"Cloning and activation of the Syrian hamster neu proto-oncogene.";

Gene 140:231-255(1994).

-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,

ALTHOUGHT NEUREGULINS DO NOT INTERACT MITH IT ALONE. GP30 IS A

POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-

C.-- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

tyrosine phosphate.

C.-- SUBMURT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
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                                                                                           AKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWM
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Mesocricetus auratus (Golden hamster).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;

Mesocricetus.

Mesocricetus.
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SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1996 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (p185erbB2) (NEU proteo-oncogene) (C-erbB-2)
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AC Q60553;
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R HSSP; P11362, 1FGK.

H RSPP; P11362, 1FGK.

R InterPro; IPR000019; EGFR L.domain.

R InterPro; IPR0001245; Furin-like.

InterPro; IPR0001245; YLP motif.

R InterPro; IPR001245; YLP motif.

R InterPro; IPR001245; YLP motif.

R Fdam; PF00155; Furin-like; 1.

R Fdam; PF01036; Recept L.domain; 2.

R Fdam; PF01036; Recept L.domain; 2.

R SWART; SM00219; TyrKc; 1.

R SWART; SM00219; TyrKc; 1.

R ROSITE; PS00107; PROTEIN KINASE ATP; 1.

R ROSITE; PS00119; PROTEIN KINASE TYR; 1.

R ROSITE; PS00119; PROTEIN KINASE TYR; 1.

R PROSITE; PS00119; PROTEIN KINASE TYR; 1.
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                                                                                                                                                                                    SFWLRVPKVSASHLENRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGCARCKGPL
                                                                                                                                                                                                  PTDCCHEQCAAGCTGPKHSDCLACLHPNHSGICELHCPALVTYNTDTFESMPNPEGRYTF
                                                                                                                                                                                                                                                                              GASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLR
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ive 59; Mismatches 100;
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DDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP 1077
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            TCSPOPEYVNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAV
                                                                                                                                     ENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGL
                                           RSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPL
                                                                                                                                                                                                                                                      EGFR HUMAN STANDARD; PRT; 1210 AA. BO6268; Q14225; Q9UMD3; Q9UMG5; Q92795; O00732; O00688; Q9ES22; Q9H2C9; Q9GSX1; Q9H3C9; Q1-196 (Rel. 01, Created) C1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor EGFR OR ERBB1.
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PUBDLINE=29708666; PubMed=8918811;
Reiter J.L., Maihle N.J.;
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"A 1.8 kb alternative transcript from the human epidermal growth
"A 1.8 kb alternative pencent of the receptor.";
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Expression of a truncated epidermal growth factor receptor-like protein (TEGFR) in ovarian cancer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=84219729; PubMed=6328312;
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Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
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Mroczkowski B., Mosig G., Cohen S.;
"ATP-stimulated interaction between epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.P.,
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MEDLINE=85046483; PubMed=6093780;
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Haley J.D., Whittle N., Bennett P., Kinchington D., Ullrich A.,
Waterfield M.D.;
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MEDLINE=84196372; PubMed=6326261;
Lin C.R., Chen W.S., Kruiger W., Stolarsky L.S., Weber W.,
Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
"Expression cloning of human EGF receptor complementary DNA: gamplification and three related messenger RNA products in A431
                                                                                                                                                                                 transcripts encoding truncated receptor
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Human and mouse alternative EGFR transcripts encoding only
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Submitted (SEP-1997) to the SWISS-PROT data bank
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MEDLINE=85270438; PubMed=2991899;
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MEDLINE=91107677; Pubmed=198848;
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Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Annu. Rev. Biochem. 56:881-914(1987).

-!- FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GPJO and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation.

-!- FUNCTION: Isoform 2/truncated isoform may act as an antagonist.
-!- CATALXTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                       Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.; "Characterization of the N-oligosaccharides attached to the atypical Asn-X-Cys sequence of recombinant human epidermal growth factor receptor.";
                                                                                                                                                                                                                                       Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F., "Analysis of the glycosylation patterns of the extracellular domain the epidermal growth factor receptor expressed in Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in ovarian cancers.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, incernalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                              tails
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TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also
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                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITES ASN-128; ASN-175; ASN-413; ASN-444
                                                                        Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M. Howk R., Givol D., Ullrich A., Schlessinger J.; "All autophosphorylation sites of epidermal growth factor (EG receptor and HER2/neu are located in their carboxyl-terminal Identification of a novel site in EGF receptor."; J. Biol. Chem. 264:10667-10671(1989).
                                                                                                                                                                                                                                                                                                                                           ASN-352; ASN-361; ASN-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: 4 isoforms, 1/p170 (shown here), truncated isoform/TEGFR, 3/p110 and 4; are produced by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE, AND DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                         CARBOHYDRATE-LINKAGE SITES ASN-56;
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MEDLINE=20198209; PubMed=10731668;
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                                                              MEDLINE=89278137; PubMed=2543678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87297456; Pubmed=3039909;
                                                                                                                                                                                                                                                                                                         Growth Factors 13:121-132(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. 127:65-72(2000)
           Nature 309:270-273(1984).
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EMBL; X00588; CAA25240.1; -. EMBL; U95089; AAB53063.1; -. EMBL; U48722; AAC50802.1; -.

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                                                                                                                                                                                         VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKD-----FNNFTVSFWLR
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                               124;
 Length 1210;
                               Indels
ch 46.2%; Score 3162; DB 1; Il Similarity 49.4%; Pred. No. 3.9e-161; 631; Conservative 177; Mismatches 345;
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BINDING
 945 MIWYKCWMIDADSRPKFRELIIEFSKWARDPQRYLVIQGDERWHLPSPTDSNFYRALMDE 1004
                                                                                                                                                                     1132 AVGNPEYLNTVQ------PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAK 1182
MIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLED 1017
                                                                       DDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP 1077
                                                                                                                                                                                                                                                                                           AVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGA 1238
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SEQUENCE FROM N.A.
STRAIN=BALB/C, and CD-1; TISSUE=Liver, and Decidua;
STRAIN=BALB/C, and CD-1; TISSUE=Liver, and Decidua;
MEDLINE=93126380; PubMed=678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                       1078 RSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVA
                                                                                                                                                                                                                    1136 PLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGG
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STRAINBE6/C3; TISSUE=Liver;
MEDLINE=94170986; PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
The mouse wared-2 phenotype results from a point mutation in the EGF
                                                                                                        1005 EDMDDOVODADEYLIPQQGFF----SSPSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ullrich A., Schlessinger J., Givol D., Morse B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93026370; PubMed=1408137;
MACOLINE=93026370; PubMed=1408137;
MACOLINE=93006370; PubMed=1408137;
Macoline region of the murine fibroblast growth factor receptor (bek/KGFR) gene.";
Oncogene 7:1957-1962(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases
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Avivi A., Lax I., Ullrich A., Sch.
                                                                                                                                                                                                                                                                                                                                                                   PPSTFKGTPTAENPEYL 1255
                                                                                                                                                                                                                                                                                                                                                                                        1183 PNGIFKGS-TAENAEYL 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes Dev. 8:399-413(1994).
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Q01279;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                        Eisinger D.P., Serrero G.; Submitted (JUL) Serrero G.; Submitted (JUL) 1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE EGE RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
-- AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphare.
                                                                                                                                                                                                                                                                                                                                               -!- SÜBCELLULAR LOCATION: Type I membrane protein.
-!- MISCELLANEOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of cell DNA
synthesis, and cell proliferation.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Kreceptor; Signal; Transferase;
Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.
SIGNAL 1 24 POTEWTIAL.
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EPIDERMAL GROWTH FACTOR RECEPTOR
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:95294; Egfr.
InterPro; IPR0000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L domain; 2.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TYrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro, IPR001245; Tyr pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U03425; AAA17899.1; -. EMBL; X59698; CAA42219.1; -.
                      binding site.";
Oncogene 6:673-676(1991).
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seq4-149-163-14.rsp

592 663 722

782

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ARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA
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Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase etbB-4 precursor (EC 2.7.1.112)
(P180erbB4) (Tyrosine kinase-type cell surface receptor HER4).
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45.9%; Score 3142; DB 1; I
Best Local Similarity 49.5%; Pred. No. 4.5e-160;
Matches 633; Conservative 171; Mismatches 358;
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                                                                                                                                                                                                                                                                              LYCOSINE PHOSPHATE.

-- SUBLUNIT: HOWDINER OF HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENITAL).

-- SUBLUNIT: HOWDINER OR HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENITAL).

--- ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B; ARE PRODUCED BY ALTERNATIVE SPLICING, THE TWO ISOFORMS DIFFER FUNCTIONALLY IN THEIR RESPONSE TO HORBOL ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.

--- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART, KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CERBBLLUM, PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS, LUNG, SALIVARY GLAND, AND PANCREAS.

--- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on itse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR000419; Euk Dkinase.
R InterPro; IPR000174; Furin-like.
R InterPro; IPR001274; Tyrin-like.
R InterPro; IPR001275; Tyrin-like.
R InterPro; IPR00149; YLP motif.
R InterPro; IPR00149; YLP motif.
R Ffam; PF001057; Furin-like; 1.
R Pfam; PF001057; Furin-like; 1.
R Pfam; PF001077; YLP; 2.
R Pfam; PF00107; PR07FIN LINASE ATP; 1.
R PROSTITE; PS00109; PR07FIN KINASE ATP; 1.
R ROSITE; PS00109; PR07FIN KINASE ATP; 1.
R ATABMEMBRAAG; Glycoprotein; Multigene family; Receptor; Signal; W Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; A Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; A Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; A Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; ATANATA.
                                                                                                                           "A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific tissue distribution and differential processing in response to photbbl ester."

J. Biol. Chem. 272:26761-26768(1997).

-!- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLUIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.

NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4. EXTRACELLULAR (POTENTIAL).
                                                                  TISSUE=Fetal brain;
MEDILINE=97476287; PubMed=9334263;
Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
Klagsbrun M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
CYS-RICH.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
                                                  SEQUENCE FROM N.A. (ISOFORMS JM-A AND JM-B)
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HSSP; P11362; 1FGK.
Genew; HGNC:3432; ERBB4.
MIM; 600543; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 IEHNRDLSFLRSVREVTGYVLVALNQFRYLPLENLRIIRGTKLYEDRYALAIFLNYRKDG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 NF------GLQELGLKNLTEILNGGVYVDQNKFLCYADTIHWQDIVRNPWPSNLTL- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 -----VST----NGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPY 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDF-----NNFTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 FWLRVPKVSASHLENRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPL
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** SE4AE80985D88761 CRC64;
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annotation update)

.5-JUN-2002 (Rel. 41, Last

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ERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNED-LGPA 1003
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                                                                           478 THLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNC
                                                                                                        SOFIRGOECVEECRVLOGIPREYVNARHCIPCHPECQP-QNGSVTCFGPEADQCVACAHY
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ERB4_RAT ID ERB4 RAT C02956; Q922N7; DT 15-DEC-1998 (Rel. 37, Created) DT 15-JUN-2002 (Rel. 41, Last sequence update)

RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1031-1198 FROM N.A. SEQUENCE SEQUENCE OF 1031-1198 FROM N.A. SEQUENCE OF 1031-1198 FROM N.A. SEQUENCE OF 1031-1198 FROM N.A. SEQUENCE OF 1031-1198 FROM N.L., Frohnert P.W., Kim S.S., Corbett J.A.; MEDLINE-97184212; PubMed=8030624; Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.; Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.; Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.; Carroll S.L., Miller M.L., Frohnert P.W., ErbB3, is induced during Wallerian degeneration."; J. Neurosci. 17:1642-1659(1997).

-!- FUNCTION: SPECIFFCALLY BINDING BGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING
NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY RECIONALIZED PATTERNS
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lai C., Lemke G.; "An extended family of protein-tyrosine kinase genes differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
             Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
ERBB4 OR TYRO-2.
                                                                                                                                                                                                                                                                 "Neuregulins promote survival and growth of cardiac myocytes.
Persistence of ErbB2 and ErbB4 expression in neonatal and adult
ventricular myocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                             Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han X., Marchionni M.A., Kelly R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESIDUES (BY SIMILARITY). SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 273:10261-10269(1998).
[2]
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InterPro; IPR000119; Euk pkinase.
InterPro; IPR002114; Furin-like.
InterPro; IPR001145; Tyr_pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00757; Purin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Sciatic nerve;
MEDLINE=91222560; Pubmed=2025425;
                                                                                                                                                                                                       MEDLINE=98221155; PubMed=9553078;
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ProDom; PD000001; Euk_pkinase; 1.
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Pfam; PF02757; YLP; Z.
                                                                           Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 848-901 FROM N.A.
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                                                          Rattus norvegicus (Rat)
                                                                                                                                                              SEQUENCE FROM N.A.
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EKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNED-L 1000
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                                                                                                                                                                                                         814 NIGSQLLIAWCVQIAKGMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEK
                                                                                                                                                                                                                                                                                                                                                                                             TGHSTLPQHAR-TPL--IAAGVIGGLFILVIMALTFAVYVRRKSIK-KKRALRRFL-ETE
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                                                                                                                                                                                                                                                                              HLREVRAVTSANIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITG
                                                                                                                                                                                                                                                                                                      SLMSAQTVDSSNIDKFINCTKINGNLIFLVTGIHGDPYNAIDAIDPEKLNVFRTVREITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFGPEADQCVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHFKDGPNCVEKCPDVLQGANSF--IFKYADQDRECHPNCTQGCNGPTSHDCIYYPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PAEQRASPLTSIVSAVV-GILLWWLGWVFGILIKRRQQKIRKYTMRRLLQETE
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  SFWLRVPKVSASHLENR - - SRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC - ARCK
                                 YLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHYKDPPFCVARCPSGVKPDLSYMPIWKPPDEEGACQPCPINCTHSCVDLDDKGC----
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                                                                                           GPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGR
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                                                                                                                                                           POTENTIAL.
RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4.
EXTRACELLULAR (POTENTIAL).
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SIMILARITY).
                     SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50010; PROTEIN—KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN—KINASE_TYR; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
25 FOTENTIAL.
26 1308 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-CHAIN
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(POTENTIAL).
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ATP (BY STMILARITY).
BY SIMILARITY.
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CYS-RICH.
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. | | | | | | | | | | 1195 ----PPKAEDEYVNEPLYLNTFTNALGNAEYMKNSLLSVPEKAKKAFDNPDYWNHSLPPR 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SWART; SM00261; FU; 5.
SWART; SM00219; TKc; 1.
SWART; SM00219; TYRC; 1.
PROSITE; PS00107; PROTEIN_KINASE ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
Tyrosine-protein kinase; ATP-binding; Phosphorylation; Proto-oncogene.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112).
XMRK OR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xiphophorus maculatus (Southern platyfish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei,
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTI
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MELANOMA RECEPTOR PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                   1251 STLQHPDYLQEYSTKYFYKQNGRIRPIVAENPEYL 1285
                                                                                           1237 GA--PPSTFKGTPT-----AENPEYL 1255
                                                                                                                                                                                                                                                                                                                    1167 AA
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InterPro; IPR000494; EGFR L domain.
InterPro; IPR000194; EGFR L domain.
InterPro; IPR002174; Furin-like.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Tyr_pkinase.
Ffam; PF001057; Furin-like; 1.
Pfam; PF001030; Recep L domain; 2.
Pfam; PF01030; Recep L domain; 2.
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                                                                                                                                                                                                                                                                                                                STANDARD;
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REVISION TO 515.
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KINASE. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). ATP (BY SIMILARITY). ATP (BY SIMILARITY). BY SIMILARITY. BY SIMI	*; Score 2690.5; DB 1; Length 1167; *; Pred. No. 4.8e-136; 165; Mismatches 385; Indels 151; Gaps AASTQVCTGTDMKLRLPASPET:LDMLRHLYQGCQVVQGN CCSTDPDRKVCQGTSNQMTMLDNHYLKMKKWYSGCNVVLEN DIOEVGGYULIAMNEVSTIPLVNLRLIRGONLYEGNFTLLDMSN GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDFNNF :
6642 116672 116672 120853 1310 111444 1114444 1114444 1114444 1114444 1114444 1114444 1114444 1114444 1114444 1114444	milarity 45.1%; Conservative 1 ALCRWGLLLALLPPGAA :
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NCBI_TaxID=9606;

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                                                                                                            IHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQ
                                                      CVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVAC
                                                                                                                                                                        AHFODGPOCIPRCPHGILGDGDTL-IWKYADKMGQCOPCHQNCTQGCSGPGLSGCRGD-I
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(C-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
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P21860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECRETED (SHORT PROM).

-! ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.
-! TISSUE SPECIFICITY: EPTTHELLAL TISSUES AND BRAIN.
-! DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROFISINS.
-! PTM: LIGAND-BINING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE PRS SUBUNIT OF PHOSPHATILINGSITOLIANS.
-! DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.
-! SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR000199; Euk_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Pfam; PF00069; pkinase; 1.
R Pfam; PF00070; Pk0071; Euk_pkinase; 1.
R Pfam; PF0010001; Euk_pkinase; 1.
R Probom; PR00101; Euk_pkinase; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
R PROSITE; PS00119; PROTEIN KINASE TYR; FALSE_NEG.
R PROSITE; PS00119; PROTEIN KINASE_DOM; 1.
R PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
R Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
M Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=90311312; PubMed=2164210; MEDLINE=90311312; PubMed=2164210; Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L., Todaro G.J., Shoyab and expression of an additional epidermal growth factor receptor-related gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Katoh M., Yazaki Y., Sugimura T., Terada M.;
"c-erbB3 gene encodes secreted as well as transmembrane receptor
tyrosine kinase.";
Bjochem. Blophys. Res. Commun. 192:1189-1197(1993)
-i- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                             Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.; "Isolation and characterization of ERBB3, a third member of the ERBB/epidermal growth factor receptor family: evide.nce for overexpression in a subset of human mammary tumors."; Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FOIENITAL).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=93282822; PubMed=7685162;
                                                              MEDLINE=90083234; PubMed=2687875;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (SHORT FORM).
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EMBL; S61953; AAB26935.1;
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Genew; HGNC:3431; ERBB3.
MIM; 190151; -.
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HSSP; P11362; 1FGK.
                                        SEQUENCE FROM N.A.
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397 YMYLSTDVGSCTLVCPLANGEVTARDCTORCERCSRECARVCGGARGAC-SREPTYDSSN 347 347 1914	RESULT 10 ERB3_RAT 1D _ERB3_RAT STANDARD; PRT; 1339 AA. AC Q627 ³ 9; Q62955;
Alternati SIGNAL CHAIN CHAIN CHAIN CHAIN DOWAIN DOWAIN DOWAIN BINDING BINDING BINDING BINDING BISULFID DISULFID CARBOHYD	OY 247 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCUTACP 306

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000194; EGFR L domain.

InterPro; IPR000194; EGFR L domain.

InterPro; IPR000119; Euk pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

R Ffam; PF00109; Pkinase; 1.

R Ffam; PF01030; Recep L domain; 2.

R FRINTS; PR010109; TYRINASE.

R PRODOM; PB000001; Euk pkinase; 1.

R PROSTIE; PS00109; TYRCT I.

R PROSTIE; PS00109; PROTEIN KINASE ATP; FALSE_NEG.

R PROSTIE; PS00101; PROTEIN KINASE DOM; 1.

R RROSTIE; PS00101; PROTEIN KINASE DOM; 1.

R PROSTIE; PS00101; PROTEIN KINASE DOM; 1.

R TAANSEMENDAME.

I TAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
DOMAIN: THE CYTOPLAENIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
PTH: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KIRASE.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 922-1097 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Sciatic nerve;
MEDLINE-ST9184212; PubMed=9030624;
MEDLINE-ST9184212; PubMed=9030624;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
"Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997).
-: FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-: CAPALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                           3.6.
15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
                                                                                                                                                                                                                                STRAIN=Sprague-Dawley; TISSUE=Liver;
BEDLINE=96096535; PubMed=852190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sterke S.L., Koland
"Cloning of the rat ErbB3 cDNA and characterization of the
                                                                                                                                                                                                                                                                                                                                                                     REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U29339; AAC28498.2; -.
EMBL; U52530; AAC53050.1; -.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                  Gene 165:279-284 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1339
                                                                                                                                                                                                                                                                                                                  recombinant protein.
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                           (c-erbB3).
ERBB3.
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119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 WLRVPKVSASHL--ENRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGC-ARCKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVRAVTSANIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LAALCRWGLLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.5%; Score 2364.5; DB 1; Length 1339; llarity 40.7%; Pred. No. 1.3e-118; Conservative 174; Mismatches 426; Indels 165; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                 CYS-RICH,
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Best Local Simi
Matches 526;
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ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFY 1011
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517
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                                                                                                                                                                                                                                        HYKDPPFCVARCPSGVKPDLSYMPIWKPPDEEGACQPCPINCTHSC--VDLDDKGCPAEQ
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                                                                                      476 HNTHLCFVHTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQC
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P04412; O61601; O9W2G0; PB1868;
13-AUG-1987 (Rel. 05, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation vector (EC 2.7.1.112) (Egfr)
16-UT COCT-2001 (Rel. 40, Dast annotation update)
16-OCT-2001 (Rel. 40, Last annotation u
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Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoc
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
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Adams ND. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams ND., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams ND., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agabayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barzendel J., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chanra I.A.
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.
RA Cherry J.M., Cawley S., Dahlke C., Busam R., Duston S., Dunkov B.C.,
RA Cherry J.M., Cawley S., Dahlke C., Ray R., Hawris M.,
ROGOR K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Busam D.M., Heiman T.J., Herman T.J., Herman T.J., Herman T.J., Herman S., Rille M., Ralush F., Karpen G.H., Re Z., Kannison J.A., Rochia C.D., Kraft C., Kravitez S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Harris M., Murphy B., Murphy L., Murphy B., Smith T.,
RA Reiner K., Remington K., Sanders R., Spiel F., Spirdling A.C., Stapleton M., Stupski M., Spier E., Spradling A.C., Stapleton M., Stupski M., Wang A., Wassarman D.A., Wang A., Wang S., Pollakor W. Sand A., Wang R., Wang Z.-Y., Wassarman D.A., Wang R., Wang R., Wang Z.-Y., Wassarman D.A., Wang R., Wang Z.-Y., Wang R., Wang Z.-Y., Wang R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [5] SEQUENCE FROM N.A. (ISOFORM TYPE I), TISSUE SPECIFICITY, AND MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99102120; PubMed=9802502;
Lesckhin A.M., Yu S.-Y., Katz J., Baker N.E.;
Several levels of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila.";
Dev. Biol. 205:129-144 (1999).
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=85124611; PubMed=2982499;
Livrah E., Glazer L., Segal D., Schlessinger J., Shilo B.-Z.;
"The Drosophila EGF receptor gene homolog: conservation of both
hormone binding and kinase domains.";
                                                                                                                                     that several genetically defined classes of alleles cluster in subdomains of the receptor protein."; Genetics 137:531-550(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE SPLICING. STRAIM-doregon-R; TISSUB-Embryo;
MEDLINE-8700-6744, Pubbed-310-310-80;
Schejter E.D., Segal D., Glazer L., Shilo B.-Z.;
"Alternative 5' exons and tissue-specific expression of the Drosophila Eff receptor homolog transcripts.";
cell 46:1091-1101(1986).
                                                                                                                                                                                                                                                                                    Clifford R., Schupbach T.;
Submitted (MAR:1998) to the EMBL/GenBank/DDBJ databases.
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                       SEQUENCE FROM N.A. (ISOFORMS TYPES I AND II)
                                                                                                                             T.;
the Drosóphila EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM TYPE I).
                                                                                                MEDLINE=94350209; PubMed=8070664;
                                                                                                                   Clifford R., Schupbach T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 40:599-607(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE III, ARE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III, ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF
TESTIS AND OVARY, AND BALN CORTEX. IN EYE-ANTENNA DISK, HICHEST
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
AND THORACIC AND ABDOMINAL GANGLIA.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97248481; PubMed=9094709;
Perrimon N., Perkins L.A.;
"There must be 50 ways to rule the signal: the case of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92038942; PubMed=1936959;
Raz E., Schejter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for
the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I. Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYFOSINE PHOSPHALE.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                MEDLINE=85137938; PubMed=298322; Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.; Prosophila genomic sequence with homology to human epidermal growth factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF052754; AAC08536.1; -.
EMBL; AF052753; AAC08536.1; JOINED.
EMBL; AF052754; AAC08535.1; -.
EMBL; AF052752; AAC08535.1; -.
EMBL; K03054; AAS1460.1; -.
EMBL; K03416; AAS1460.1; -.
EMBL; K03416; AAAS0965.1; -.
                                                                                                                                                                                                                                                           SEQUENCE OF 959-1078 FROM N.A. STRAIN=Daekwanryeong;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 314:178-180(1985).
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83 YVLIAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASPGGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDF-NNFTVSFW----LRVPKVSASHLEN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 TDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT-NASLSFLQDIQEVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 --RECPKCHESCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 GPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 RDNGACVRSCPQDKMDKGGE-----CVPCNGPCPKTCPGVTVLH-----AGNIDSFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 470; Conservative 190; Mismatches 422; Indels 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPIDERMAL GROWTH FACTOR RECEPTOR. EXTRACELULAR (POTENTIAL). POTENTIAL.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
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Prodom; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 7.
PROSTTS; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                 AR109078; AAD26133.1; AR109078; AAD26133.1; JOINED. AR109084; AAD26130.1; JOINED. AR109081; AAD26130.1; JOINED. AR109081; AAD26130.1; JOINED. AR1090803; AAD26131.1; AR1090803; AAD26131.1; AR1090803; AAD26131.1; AR1090804; AAR46722.1; AR10918; CAAS5521.1; AR10918; CAAS5521.1; AR10918; CAAS5521.1; AR10919; CAAS5522.1; AR10918; 
                                                                                                                                                                                                                                                                                                PIR; A00640; GQFFE.
HSSP; P11362; 1FGK.
FlyBase; FB901001731; Egfr.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR00119; Buk pkinase.
InterPro; IPR001214; Furin-like.
InterPro; IPR00124; Furin-like.
Pfam; PF00169; Pkinase; 1.
Pfam; PF001030; Recept L domain; 2.
                                                                                                                                                                                                                                                                                                                                                                              domain
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868
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SIGNAL 1
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869
890
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44;

82

255

251 312 311 371 423

AF109077; AAD26134.1; -. AF189078; AAD26132.1; -.

EMBL; EMBL; EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.

-I- MISCELLANBOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS
IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS
AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY
THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE
C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

-I- MISCELLANBOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.5%; Score 1749.5; DB 1; Length 634;
52.3%; Pred. No. 3.1e-86;
iive 79; Mismatches 135; Indels 123; Gaps
                               21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                     Cell 41:719-726(1985).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A00643; TVCHLV.

R PIR; A00643; TVCHLV.

R HSSP, P11362; TVCHLV.

HICEPPO: IPR000719; Buk_pkinase.

R InterPro: IPR001245; Tyr_pkinase.

R PRINTS; PR00109; pkinase; 1.

R PRINTS; PR00109; TyrKC; 1.

R PRART; SM00219; TyrKC; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS0011; PROTEIN KINASE DOM; 1.

M TRANSE TARE: DS0011; PROTEIN KINASE DOM; 1.

M TRANSE TARE: DS0011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                            MEDLINE=85228222; PubMed=2988784;
Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
Crittenden L.B., Raines M.A., Kung H.-J.;
"c-erbs activation in ALV-induced erythroblastosis: novel
processing and promoter insertion result in expression of
amino-truncated EGF receptor.";
                                                                                                                                          Viruses, Retroid viruses, Retroviridae, Alpharetrovirus NCBI_TaxID=11864,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70891 MW; E705E33A0BE01FCC CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
   634 AA
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PRT;
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STANDARD;
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165
257
                                                                                                                         Avian leukosis virus.
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712 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK 771

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Glycoprotein;
DOMAIN 13
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                                                                                                                                                                                                      PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1125
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                                                                      417
           177
                                             237
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SEQUENCE OF 1-152 FROM N.A.

MEDLINE=84223957; PubMed=6328658;

MEDLINE=84223957; PubMed=6328658;

Saule S., Martin P., Stehelin D.;

"Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of oncogene.";

"Sequencing the Acrivity ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

1- OISEASE: THE V-ERBB ONCOCENE TRANSFORMS AVIAN FIBROBLASTS AND IN CHICKENS.
YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
                                                                                                                                                                             LPSET - - DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK
                                                                                                                                                                                                                                                  NGVVKDVF-------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY
                                                             CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                              I KWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                                                                                                                                                                                                    K.;
                                                                                                                                                                                                                                                                                                                                                                                                                               Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=79685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima "The erbB gene of avian erythroblastosis virus is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112) V-ERBB.
                                                                                                                                                                                                                                                                                                            WDO------DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1260
                                                                                                                                                                                                                                                                                                                            579 WIOSGNHOINLDNPDYQODFLPNETKPNGLLKVPAAENPEYLRVAAP 625
                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=H;
MEDLINE=84026539; PubMed=6313229;
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P00535;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
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                                                                                                                                                                                                                                                                      R EMBL; K02006; AAA42394.1; ALT_INIT.
R PIR; A00644; TVYUH.
R PIR; A00644; TVYUH.
R INTERPO; IPRO00719; Euk_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Prodom; P0000601; Euk_pkinase; 1.
SMART; SM00219; TyrKc; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00119; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 126;
-!- MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION RECEPTOR FOR EPIDERMAL GROWTH FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.9%; Score 1703; DB 1; Length 604; 52.2%; Pred. No. 8.7e-84; ive 76; Mismatches 128; Indels 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R -> W (IN REF. 2).
S -> F (IN REF. 2).
I -> V (IN REF. 2).
76EBCDD06745D609 CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Best Local Similarity 52.2*
Matches 360; Conservative
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604 AA;
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                                                                                1184 NGVVKDVFAF---------GGAVENPEYLTPQGGAAPQPHPPPAFSPAFD 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                  ----SRTPLLSSLSATSNNSATNCID-----RNGQGHPVREDSFVQRYSSDPTGN 495
                           1126 LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK
                                                                                                                                                                                                                                                                                                                                                                         [1] -
SEQUENCE FROM N.A.
MEDLINE=87064458; PubMed=2878364;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbB confers a thermolabile
phenotype to t8167 avian erythroblastosis virus-transformed erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                        Avian erythroblastosis virus (strain ts167).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=103898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Cell. Biol. 6:1751-1759(1986).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                        erbB (EC 2.7.1.112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.8%; Score 1630; DB 1; Length 54(55.1%; Pred. No. 5.9e-80;
ive 69; Mismatches 119; Indels
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5B53297AA068B65D CRC64;
                                                      496 FLEESIDDGFL-----PAPEYVNQ--LMPKKPSTAM----
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PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding;
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(BY SIMILARITY)
                                                                                                                                                                                                                                                P11273;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                     Tyrosine-protein kinase transforming protein
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InterPro, IPR00119; Euk pkinase.
InterPro, IPR001245; Tyr pkinase.
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ProDom; PD000001; Euk pkinase; 1.
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Matches 341; Conservative
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BINDING
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Mol. Cel
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CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ 652

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 58
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                                                                            MPNOAOMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                                                                                                                  CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                         RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQOKIRKYTMRRLLLQETELVEPLTPSGA
                                                                                                                                                                                                                                     892 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                                                                                                                                                                                                                                                           1011 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-UJN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (CER)
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
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NCBI_TaxID=9031;
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13 RGAAVLVLLLLGVALCSAVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLE LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD 122 PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDFNNFTVSFWL 133 -MNKTQ-----GLRELPMKRLSEILNGGVKISNNPKLCNMDTVLWNDIIDTS----192 RVPKVSASHLENRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTD

121

181

178 240 237 297 360 356 420 416 480 476 540 536 597

CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS 300

179 241 361 AVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISA

357

421

481 477

WPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHL

CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR

301

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                                 DNA
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R InterPro; IPR00019; Euck pkinase.
R InterPro; IPR00119; Euck pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Pfam; PF001019; Furin-like; 1.
R Pfam; PF001019; PROTEIN KINASE ATP; PARTIAL.
R PROSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.
R PROSITE; PS00109; PROTEIN KINASE DOM; PARTIAL.
TYCOSING-Protein Kinase; ATP-binding; Phosphorylation.
I TYCOSING BY STORELULAR (POTENTIAL).
T CHAIN 31 < 654 POTENTIAL.
T DOMAIN 31 654 POTENTIAL.
T DOMAIN 655 667 POTENTIAL.
T DOMAIN 197 206 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPIDERMAL GROWTH FACTOR RECEPTOR
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SEQUENCE
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completed: July 22, 2003, 08:44:56 te : 22.2793 secs time

657 652

DPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPL DGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---NGSKT

598

TSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP 708

658

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541 LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAHYK

CFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQF

61

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Gaps

RWGLLLALLPPGAA----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE

seq4-149-163-14.rspt

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July 22, 2003, 08:22:34; Search time 48.5887 Seconds (without alignments) 5347.444 Million cell updates/sec
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6848
1 MELAALCRWGLLIALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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7: sp_mhc:*
7: sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O18735 canis famil	Q9qx70 rattus norv	Q9ep98 mus musculu	O9vh40 xiphophorus	O9w6f6 gallus gall	P79754 fugu rubrin	Osbihe anopheles o	Oguk79 homo sapien	O8r2x1 mus musculu	086712 avian rous-	086714 avian rous-	O8wvv0 homo sapien	064895 avian ervth	O85468 avian prvth	Control of the contro	Q9erv6 mus musculu
SUMMARIES	ΩI	018735	090X70	Q9EP98	Q9YH40	Q9W6F6	P79754	69вінэ	Q9UK79	Q8R2X1	086712	086714	QBWYVO	Q64895	085468	O9WVFS	Q9ERV6
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oks	Query Match	90.5	46.2	45.8	39.8	39.6	33.7	29.9	26.0	25.4	25.1	25.1	24.8	24.1	24.0	22.3	22.1
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ALIGNMENTS

RESULT 1 018735) 018735 PRELIMINARY; PRT; 1259 AA.		01-JAN-1998 (TrEMBLrel. 05,		ErbB-2.	Canis familiaris (Dog).	Eukaryota; Metazoa;	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;	NCBI_TaxID=9615;	•	•	Yokota H.;	"CDNA cloning of		EMBL; AB008451; E		InterPro; IPR002048;	InterPro; IPR000494;		InterPro; IPR002174;	InterPro; IPR001245;	InterP	Pfam; PF00757; Furin-	Pfam; PF00069; pkinase; 1.		Pfam; PF02757; YLP; 2.	ProDom;	SMART; S	SMART;	PROSITE, PS00018; EF HAND	PROSITE, PS00107;	PROSITE; PS50011;	PROSITE; PS00109; PROTEIN	ATP-binding; Trans	SEQUENCE 1259 AA; 1379
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"A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively spliced transcript in normal rat tissue."; Mol. Cell. Biol. 10:2973-2982(1990).
                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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R HSSP; P11362; 1FGK.

R HSSP; P11362; 1FGK.

R HSSP; P11362; 1FGK.

R InterPro; 1PR000149; Euk pkinase.

R InterPro; 1PR000144; Furin-like.

R InterPro; 1PR00144; Furin-like.

R InterPro; 1PR00145; Tyr pkinase.

R Fdam; PF00157; Furin-like; 1.

R Fdam; PF00169; pkinase; 1.

R Pfam; PF00109; Recep_L domain; 2.

R PRINTS; PR00109; TYRKINASE.

R PROSTITE; PS00101; PROTEIN KINASE ATP; 1.

R PROSTITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSTITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSTITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSTITE; PS00109; PROTEIN KINASE TYP; 1.

R PROSTITE; PS00109; PROTEIN KINASE TYP; 1.

R PROSTITE; PS00101; PROTEIN KINASE TYP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                             090X70 PRELIMINARY; PRT; 1209 AA.
090X70;
01-MAX-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
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Pred. No. 5.2e-230;
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STRAIN=FISHER, TISSUE=LIVER,
Guttridge K., Dawson T.L., Earp H.S.;
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Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
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STRAIN=FISHER; TISSUE=LIVER,
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Local Similarity
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                                                                                                                                          ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                                                                                                                                                 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDF---NNFTV 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LESIPPRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
                                                                                           MELAAWCRWGLLLALLPSGAAGTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                     DPLEGGIPAPGAAQGGLRELQLRSLTEILKGGVLIQRSPQLCHQDTILWKDVFHKNN---
                                                                                                                                                                                                                                                                                      SFWLRVPKVSASHLE-NRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGP
                                                                                                                                                                                                                                                                                                          LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT
                                                                                                                                                                                                                                                                                                                                                                               231 QPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSQFLRGQECVEECRVLQGLPREYVKDRYCLPCHSECQPQNGSVTCFGSEADQCVACAHY
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                                                                        MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                       Gaps
                                     20;
   Length 1259;
                                   Indels
                                   58;
   DB 6;
; Score 6198; D)
; Pred. No. 0;
44; Mismatches
 90.5%; Score
90.4%; Pred.
Query Match
Best Local Similarity 90.4%
Matches 1148; Conservative
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; <u>8</u>		đ	1084 TFL
ò	PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDFNNFTVSFWL	È	1192 AFGGAV
QQ		qo	1127 PHSNAV
ò	ENRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RC	È	
QQ	168 -VQDVFLSNMSMDVQRHLTGCPKCDPSCPNGSCWGRGEENCOKLTKIICAQQCSRRCRGR 226	ପ୍ଧ	1178 KEAKPNO
ò	237 LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT 296	RESULT	JLT 3
QQ	227 SPSDCCHNQCAAGCTGPRESDCLVCHRFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYS 286	362	OSEPS8 PREI
ò 8	297 FGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHL 356	488	01-MAR-2001 (Tri 01-MAR-2001 (Tri
	GALLVANLFRINT VYIDROSLVKALGFUTIEV - BEDGVSKLKKLUGFURGEFURGEF	9 B	01-JUN-2002 (Tri Epidermal growth
% 49	33. REVANTATION RECONSTRUCTION FOR THE STRUCTURE OF THE S	N O O	EGFR. Mus musculus (Mo
		888	Eukaryota; Metaz Mammalia; Euthez
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	NEUT CONDENOT DONDUCAT UNA AND DEDICACIONAL ACTOR A CONTRACTOR ACTOR AND ACTOR AND ACTOR AND ACTOR AND ACTOR	R R	SEQUENCE FROM N STRAIN=C3H/101,
	NITHELY WILLY WIND THE THE TANK THE THE TANK THE	8 8	Reiter J.L., Thr Sinclair C.S., E
	NEW DUTANT INVANCE OF FINGEL BETWEEN THE TOTAL OF THE SECUNG PEPTD CVS	8 8	Balasubramaniam Maihle N.J.;
	537 CSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHY 596	RT	"Comparative ger
	526 CQNVSRGRECVDKCNILEGEPREFVENSECIQCHPECLPQTMNITCTGRGPDNCIKCAHY 585	RT	isoforms.";
ò	597 KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP 656	R S	[2]
qa	586 VDGPHCVKTCPSGIMGENNTL-VWKFADANNVCHLCHANCTYGCAGPGLKGCQQPEGP 642	RP	SEQUENCE FROM N. STRAIN=C57BL/6J
'n	657 -LTSIVSAVVGILLVVVLGVVFGI-LIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPN 714	2 2	Reiter J.L., Thi Schehl C., Pears
qq	643 KIPSIATGIVGGLLFIVV-VALGIGLFWRRRQLVRKRTLRRLLQERELVEPLTPSGEAPN 701	8 8	Balasubramaniam Maihle N.J.:
ò	715 OAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEIL 774	RT	"Comparative ger
qa	: :	RL	isoforms."; Submitted (TIN-2
ćo		S S	EMBL; AF275366; EMBL; AF275364
qq		90 S	EMBL; AF275365; EMBL; AF275367;
ò	835 IAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKW 894	DR DR	HSSP; P11362; 1F MGD; MGI:95294;
qq		<u>қ</u> қ	InterPro; IPR000 InterPro; IPR000
ò	895 MALESILRRRPTHQSDVWSYGVTVWELMTFGAKRYDGIPAREIPDLLEKGERLPQPPICT 954	DR DR	InterPro; IPR000 InterPro; IPR002
q ₀	882 MALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPPICT 941	8 8	InterPro, IPR002 InterPro, IPR001
٥, ٥	955 IDVYMIMVKCWMIDSECRPRFRELVSEPSRMARDPORFVVIQ-NEDLGPASPLDSTFYRS 1013	* # K	Ptam; PF00757; F Pfam; PF00069; p Pfam; PF01030; R
		e e	PRINTS; PR00109;
	LLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSE : : : : : : :	888	SMART; SM00261; SMART; SM00220;
	1002 LMEEEDMEDVVDADEYLIPQQGFFNSPST 1030	DR	SMART; SM00219;

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LTCSPOPEYVNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVF 1191
                                                                                                                    VSNPEYLNTAQ------PTCLSSGFDSSALWIQKGSHQMSLDNPDYQQDFFP 1177
SPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--D 1131
                                                                                                                                                                                       VENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----P 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
129/SVJ, AND 129/SVEVTAC;
ffreadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
am S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hreadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., reall R.S., Green P.J., Yee D., Lampland A.L., m S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              azoa, Chordata, Craniata, Vertebrata, Euteleostomi,
eria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
90,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enomic sequence analysis and isolation of human and ive Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enomic sequence analysis and isolation of human and ive Egfr transcripts encoding truncated receptor
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rEMBLrel. 16, Last sequence update)
TEMBLrel. 21, Last annotation update)
th factor receptor isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1210 AA.
                                                                                                                                                                                                                                                                                PSTFKGTPTAENPEYLGLDVP 1260
                                                                                                                                                                                                                                                                                                                000345; CytC heme bind.
000494; EGFR L domain.
000719; Euk pkinase.
002174; FvrIn-like.
002290; Ser thr pkinase.
001245; Tyr pkinase.
; Furin-like; 1.
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AAG28045.1; JOINED.
AAG28045.1; JOINED.
AAG24386.1; -.
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; Recep_L domain; 2.
09; TYRKILASE.
001; Euk_pkinase; 1.
1; FU; 5.
9; STKC; 1.
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1011 bvvbadevirpooger----skrpl 1036
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                                                                                                                                                                                                                                                                                                                              1136 PEYLNTAQ-----PTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPNGI 1186
                                                   1082 APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTC
RIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIMV
                                KCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMG
                                                                                               DLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPL
                                                                                                                                                                                  LSSLSATSN----NSTVACINRNGSCRVKEDAFLQRYSSDPTGAVTEDNIDDAFL----
                                                                                                                                                                                                                              1140 SPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVEN
                                                                                                                                                                                                                                                                                               PEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----DP----PERGAPPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xiphophorus xiphidium.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
1015_TaxID=8086;
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Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=RIO PURIFICATION;
STRAIN=RIO PURIFICATION;
MEDLINE-9241172;
Dimitrijevic N., Winkler C., Wellbrock C., Gomez A., C.
Alteschmied J., Schartil M.;
Activation of the Xmrk proto-oncogene of Xiphophorus
overexpression and mutational alterations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep__domain; 2.
Propom; PF00109; TYRKINASE.
ProDom; PF000001; Euk_pkinase; 1.
SMART; SM00219; TYRC; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS001303; GRAM_POS_ANCHORING; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor tyrosine kinase proto-oncogene.
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InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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InterPro; IPR0000494; EGFR_domain.
InterPro; IPR000719; Eux pkinae.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                1243 FKGTPTAENPEYLGLDVP 1260
                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
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HSSP; P11362; 1FGK.
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                                                                                                                                                 Gaps
                                                                                                                                               Indels 116;
                                                                                                               Length 1210;
                                                                                   CRC64;
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Receptor; Transferase.
SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18
                                                                                                               / Match 45.8%; Score 3139; DB 11;
Local Similarity 49.5%; Pred. No. 5.7e-228;
Heb 633; Conservative 170; Mismatches 359;
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                                                                                                                                                                        56 VQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALA
                                                                                                                                                                                                                                       - NNFTVSFWLRVPKVSASHLENRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-
                                                                                                                                                                                                                                                                                        174 TSNPTMNL---IPHAF------ERQCQKCDPGCVNGSCWAPGPGHCQKFTKLLCAEQCN
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                                                                                                                         1 MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
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                                                                                                    Gaps
                                                                        Query Match 39.8%; Score 2724; DB 13; Length 1165; Best Local Similarity 45.5%; Pred. No. 1.2e-196; Matches 583; Conservative 165; Mismatches 380; Indels 154;
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SEQUENCE 1165 AA; 129614 MM; 7F7EE38D8771A74E CRC64;
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        1070 EPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPS
                                                                                             1176 AKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPE
                                                                                                                             -----YQAAF-----LPQ
                                                                      ------PVRENSIALRYISDPTQNALEK
                                                                                    ETDGYVAPLTCSPQPEYVNQPDVRPQP-----PSPRE-----GPLP-AARPAGATLER
                           1010 FYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGL
                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Receptor tyrosine kinase (Fragment).
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                                                                                                                             1100 PEYLNTNONSL---PLVSSGSMDDPDY---QAG-
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                                                                      ------EPCIPPNGH-------
                                                                                                                                          RGAPPSTFKGTPTAENPEYLGL 1257
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13; Length 1137;

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39.6%; Score 2711.5;

Query Match

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Genome Res. 9:251-258(1999).
EMBL; AF056116; AAC34391.1;
HSSP; P11362; 1FGK.
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SMART; SM00219; TYTKC; 1.
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                                                                                    LCFADTIHWQDIVRNPWASNFTL----VP----TNGSSGCGRCHKSCTG-RCWGPT
                                                                                                                          215 SEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELH
                                                                                                                                             ENHCQTLTKTVCAEQCDGRCYGPYVSDCCHRECAGGCSGPKDTDCFACMNFNDSGACVTQ
                                                                                                                                                                                                                  CPQTFVYNPTTFQLEHNHNAKYTYGAFCVKKCPHNFV-VDSSSCVRACPSSKMEV-EENG
                                                                                                                                                                                                                                                                   TORCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPAS
                                                                                                                                                                                                                                                                                        168 IKMCKPCTDICPKACDGIGTGSLVSAQTVDSSNIDKFINCTKINGNLIFLVTGIHGDPYH
                                                                                                                                                                                                                                                                                                                                         NTAPLOPEQLOVFETLEEITGYLYISAWPDSLPDLSVFONLOVIRGRILHNGAYSLTLQG
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                                                                                                                                                                                               CPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDG
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                Gaps
                95;
Pred. No. 1e-195;
); Mismatches 346; Indels
             170;
46.98;
                540; Conservative
Best Local Similarity
Matches 540; Conserv
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EYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGA--PPSTFKGTPT----- 1248
                                                                             EENPFVSRRKNGDLQAVDNPEYHN----APNGQPKAEDEYVNEPLYLNTFANTLENA 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                      Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Ekkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fugu
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MEDLINE=99177347; PubMed=10077531;
Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA around the wntl locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148613 MW; A333039258B647E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                       01-WAY-1997 (TrEMBLrel. 03, Created)
01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
ExbB3.
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SEQUENCE 1328 AA; 148613 MW; A3330
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InterPro; IPR000194; Euk pkinase.
InterPro; IPR00174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00057; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF001030; Recep L domain; 2.
Probom; PF000001; Euk pkinase; 1.
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FGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQR - CEKCSKPCARVCYGLGMEH
                                                                                      LYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIH
                                                                                                                                               ONAHLCYHHTVNWTQLFRGSRVRANSLNSNRPMAECVADGRVCDPLCSDSGCWGPGPDQC
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                                                                                                                                  HNTHLCFVHTVPWDQLFRNPH-QALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1433;
                                                                                                                                                                                                          "Cloning, expression and localisation of the Anopheles gambiae epidermal growth factor receptor."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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1433 AA; 159585 MW; E3D9D88967724F07 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
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29.94; Score 2017.2, 2. Best Local Similarity 32.74; Pred. No. 2e-145;
Matches 476; Conservative 195; Mismatches 389;
                                                                                                                                                                                                                                                                               InterPro; IPR000145; CytC heme bind.
InterPro; IPR000145; CytC heme bind.
InterPro; IPR000149; EGFR L domain.
InterPro; IPR001749; Euk Dyfnase.
InterPro; IPR001249; Set Lhr Dyfnase.
InterPro; IPR001245; Tyr Dyfnase.
InterPro; IPR001245; Tyr Dyfnase.
Fam; Pr000057; Furin-like; 1.
Pfam; Pr001057; Furin-like; 1.
Pfam; Pr00109; Recept L domain; 2.
ProDom; PR001009; TYRRINASE.
ProDom; PR001009; TYRRINASE.
INTE; SM001201; Euk Dyfnase; 1.
SWART; SM001201; TyrKC; 1.
SWART; SM001201; TYRC; 1.
PROSITE; PS00119; PROTEIN KINASE DOM; 1.
PROSITE; PS00110; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                      EMBL; AJ301655; CAC35008.1;
HSSP; P11362; 1FGK.
                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=SUA;
                                                                                                                                   NCBI_TaxID=7165;
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NON TER
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                                        PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
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                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                              [1] SEQUENCE FROM N.A.
MEDIINE=99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER.2/neu receptor tyrosine kinase gene encodes a secreted autoinhibitor.";
                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 419;
                                                                                                                                                                                                                         Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner is Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR00494; EGFR L domain.
InterPro; IPR002174; Furin-Tike.
Pfam: PF01030; Recep L domain; 1.
SMART; SM00261; FU; I.
SEQUENCE 419 AA; 45472 MW; FECIBE347E2D030C CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874 (1999)
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01-JUN-2002 (
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MEDLINE=94203659; PubMed=8152791;

Wendstrom B., Raymoscheck C., Jansson L., Doederlein G., Lhotak V., Johnsson A., Baug H.;

"Retroviral capture of c-erbB proto-oncogene sequences: rapid evolution of distinct viral genomes carrying mutant v-erbB genes with different transforming capacities.";

Oncogene 9:1307-1320(1994).

EMBL; S69372; AAG6025:1; -.
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                            DB 11; Length 367;
                                                                                                                                                                                                                                                                                     33; Indels
                                                                                                                    Strausberg R.; Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC027080; ART7080.1; -. Hypothetical protein. SEQUENCE 367 AA; 40163 MW; OBE03395F9E101B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avian rous-associated virus type 1.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
VCBI_TaxID=11950;
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Last annotation update)
                                                                                                                                                                                                                                          Query Match 25.4%; Score 1739; DB 11, Best Local Similarity 88.0%; Pred. No. 5.4e-123, Matches 323; Conservative 11; Mismatches 33;
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InterPro; IPR004028; Retro M.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
Pfam; PF02813; Retro M; I.
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musculus (Mouse)
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LGLDVPV 367
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                                                      NCBI_TaxID=10090;
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MEDIINE=94203659; PubMed=8152791;
Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
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                                                                                                                                            Length 729;
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
              SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

ATP-binding; Transferaee; Tyrosine-protein kinase.

SEQUENCE 729 AA; 80649 MW; 84D2P6914EFEID63 CRC64;
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Last annotation update)
                                                                                                                                            DB 15;
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ProDom; PD000001; Euk_pkinase; 1.
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              with
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        sequences: rapid
mutant v-erbB genes
                                                                                                                              tch 25.1%; Score 1718; DB 15; Length 567; al Similarity 55.4%; Pred. No. 4e-121; 357; Conservative 73; Mismatches 112; Indels 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                               ----TAMVQNQIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL 566
                                                                                                                 567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
Query Match
Best Local S
Matches 357
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PRT;

PRELIMINARY;

QBWYV0 QBWYV0; RESULT 12 QBWYV0 ID QBWYV AC QBWYV

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955 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL 1014
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                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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80.5%; Pred. No. 8.8e-120;
ive 5; Mismatches 22; Indels 53;
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                                                                                                                                                                                                                                                                                                                                    (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 412 AA; 44702 MW; 034397FF3F27D2BC CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gag, V-erb-A, v-erb-B protein.
GAG, V-RR-A, V-ERB-B.
Avian erythroblastosis virus.
01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mypothetical 44.7 kDa protein.
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PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                            Huang Y., Zhou X.M., Zhang P.P., Jiang Wan D.F., Gu J.R.;
                                                                                                                                                                                                                                                                                                                                                    EMBL; AF318349; AAL55856.1; ...
InterPro; IPR002048; EF-hand.
InterPro; IPR00119; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YuP_motif.
Pfam; PF00669; pkinase; Ţ.
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SMART; SM00219; TyrKc; 1.
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Matches 330; Conservative
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SEQUENCE FROM N.A.
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Submitted
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354 IEKCQESYLLAFEHYINYRKHNIPHFWSKLLMKVADLRMIGAYHASRFLHMKVECPTELS
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                            MEDLINE-90206603; PubMed=1969616;

MEDLINE-90206603; PubMed=1969616;

MEDLINE-90206603; PubMed=1969616;

MEDLINE-90206603; PubMed=1969616;

MEDLINE-90206603; PubMed=1969616;

MEDLINE-90206603; PubMed=1969616;

L. Signation and the retroviral gene gag greatly enhance the transforming potential of the oncogene v-erb-B.";

L. Concogene 5:15-24(1990).

C. -- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C. -- SUBCELLULAR LOCATION: NUCLEAR HORMONE RECEPTORS FAMILY.

REMBL; X522109; CAA36459-1; JOINED.

R EMBL; X52211; CAA36459-1; JOINED.

R InterPro; IPR000719; EUK_pkinase.

R InterPro; IPR001723; Fullman_receptor.

R InterPro; IPR00173; Fullman_receptor.

R InterPro; IPR00173; Fullman_receptor.

R InterPro; IPR00163; ZfC (4steroid.

R Pfam; PF000104; hormone_rec; 1.

R Pfam; PF000105; Zf-G4; 1.
                                                                                                                                                                                                                                                     R PRINTS, PR00398; STRCHORMONER.
R PRINTS; PR00047; STRCIDFINGER.
R Prodom; PD000001; Euk_pkinase; 1.
R Prodom; PD000015; Znf_C4steroid; 1.
SWART; SM00430; HOLI; 1.
R SWART; SM00139; Znf_C4; 1.
R SWART; SM00139; Znf_C4; 1.
R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
R PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.
R PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.
R ATP-binding; DNA-binding; Nuclear protein; Receptor; 1.
R Transcription regulation; Transferase; Tyrosine-protein kinase;
                                                         R.C.
Retroid viruses; Retroviridae; Avian type C retroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 24.1%; Score 1653.5; DB 15; Length 962; Il Similarity 51.7%; Pred. No. 6.5e-116; 358; Conservative 73; Mismatches 142; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 VEECRVLQGLPRE-YVNAR-HCLP-------
                                                                                                                                                                                                                                                                                                                                                                                                                       962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
Viruses, Retroid v
NCBI_TaxID=11861;
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VIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHR 1052
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                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=88217326; PubMed=2897102;
MEDLINE=88217326; PubMed=2897102;
Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.;
Common site of mutation in the erbB gene of avian erythroblastosis
virus mutants that are temperature sensitive for transformation.";
Oncogene Res. 1.265-278(1987).
EMBL; X06943; CAAA30024.1; -.
HSSP; P11362; 1FGK.
                                                                                                                                                                                        1113 SPLORYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703 VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      644 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
4 vian Erythroblastosis virus (Te34) v-erbB gene.
Avian erythroblastosis virus.
Viruses, Retroid viruses, Retroviridae, Avian type C retroviruses.
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                      140DCE8CCA0FBAF4 CRC64;
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InterPro; IPR001245; Tyr_Dkinase.
InterPro; IPR001245; Tyr_Dkinase.
Promom; P0000601; Euk_Dkinase; 1.
Prodom; P000001; Euk_Dkinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
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                                                                                                                                                                                                                                                                                      1173 -LERAKTLSPGKNGVVKDVFAFGGAVENPEYL 1203
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                                                                                                                                                                       GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1116
                                                                                                                                                                                                                              117 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1175
                                                                                                              PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1061
                                                                                                                             294 YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE 353
                                                                                                                                                                                                                                                 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
                                                      KGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATRAIN-CS7BL/6J; TISSUE-LIVER;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Marsuo Y., Nikaido I., Pesole G. Quackenbush J.,
Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
                                                                                                                                                                                      354 KGERLPQPPICTIDVYMIMVKCWMSDADSRPKFRELIAEFSKMARDPPRYLVIQGDERMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
Maihle N.J.;
"Alternative Transcripts from the Human and Mouse EGFR Genes Encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balagubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                       1176 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1203
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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wingham, Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human herequlin 2	Human tyrosine kin	HER2 transgene pla	Human HER2 (ErbB2)	HER-2/neu protein.	Human HER-2/neu on	Human HER-2/neu pr	Amino acid seguenc	Human HER-2/neu pr	HER2/neu amino aci
SUMMARIES			ID		AAE12130	AAB60167	AAU74545	AAW01111	AAW92406	AAB21198	AAY84780	AAB85458	AAG88267
			DB	21	22	22	23	11	20	21	21	22	22
			e Match Length DB	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255
	من	Query	Match	98.1	98.1	98.1	98.1	98.0	98.0	98.0	98.0	98.0	98.0
			Score	6715	6715	6715	6715	6109	6109	6209	6109	6109	6009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the human heregulin 2 (Her2) sequence. Immunogenic analogues Her2 can be used in the claimed method as an autovaccine to induce a response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign helper epitopes were identified (see features table). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
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cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PA), hereagalin Z (Herz) and/or fibroblast growth factor 80 (FGFBb). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA, and (2) at least 1 B-cell group derived from the GFBb comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitopes of the respective PA and including at least to foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSW, FGFBb and Her2, respectively.
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducting an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines characterised by expression of the breast cancer antigen, HER-2. Polymucleotides that encode peptides of the invention are useful ase transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polymucleotides into host cells. The present confirm transduction of polymucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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                                                  KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDI
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                                                                                               The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbBs (also known as HER2 and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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                                     Treating tumors, particularly breast cancers, which overexpress ar receptor and does not respond to an anti-ErbB antibody, comprises conjugating the antibody to a maytansinoid -
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                                      AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLAWCMQIA
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LTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
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16-MAR-2000; 2000US-0189844.
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                                                                                       LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 956
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ovar stomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; pithelial disorder; stromal disorder; plastocoalic disorder; inflammatory disorder; anglogenic disorder; inflammatory disorder;
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05-OCT-2000; 2000US-238327P.
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SCHWALL R.
SLIWKOWSKI M.
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                                                                                                   Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
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Sliwkowski M;
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Matches 1242; Conservative
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Schwall R,
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/label= Intracellular_domain
/note= "claimed domain, useful for immunisation"
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                                                                                                                                                                                                                                                                Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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Best Local Similarity 98.0%; Pred. No. 0;
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This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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98.0%; Pred. No. 0;
iive 7; Mismatches 4;
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96US-0625101.
93US-0033644.
93US-0106112.
95US-0414417.
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The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against these neoplasias.
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                                           QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE
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                                                                                        Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
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                                                                                       QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE
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The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated Specifically, these are useful for treating or preventing cancer. e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as pl85 or c-erbB2).
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                                                  New antigen-presenting cells, useful as vaccines for eliciting o
enhancing an immune response to HER-2/neu protein, particularly
for treating or preventing cancer, e.g. breast cancer
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iive 7; Mismatches
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Matches 1240; Conservative
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                                          LTSIISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
                                                                      AYVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
                                                                                                                          LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
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LTSIISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA 710
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immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                               VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLE
                                                                                                                                                                                                                 DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEA
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The present invention describes isolated prepared HER2/neu epitopes (1).

Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is

CC chilture in vitro and binds to a complex of an epitope (1), bound to a

Chuman leukocyte antigen (HLA) molecule; (2) a peptide (11) comprising (1)

and a second epitope and the peptide is less than 50 contiguous amino

cc acids that have 100% identity with a native peptide sequence of HER2/neu;

(3) a vaccine composition (III) comprising (II) and a pharmaceutical

CC axipient; (4) an isolated nucleic acid encoding a peptide comprising

(1); and (5) an isolated nucleic acid encoding (II). (1) has cytostatic

and immunostimalant activities, and can be used in vaccines. (1), (II)

and (III) are useful for inducing cellular immune responses for the

prevention and treatment of cancer. (1) and (II) are useful for

and immunostiming an immune response to a tumour-associated

antigen when incubated with a T lymphocyte to (1) or (II). Epitope

conting the presence of bound T lymphocyte to (1) or (II). Epitope

conting the presence of bound T lymphocyte to (1) or (II). Epitope

conting man be any be avoided. Selected epitopes that may be present

in whole antigens may be avoided. Selected epitopes that may be present

contines the ability. The possible pathological side effects caused by

infectious agents or whole protein antigen is eliminated. The vaccine

provides the ability to direct and focus an immune response to omultiple

contines provides the opportunity to combine epitopes derived from

multiple tumour-associated molecules addressing the problem of tumour-

cumulciple tumour-associated molecules addressing the problem of tumour-

cumulciple tumour-associated molecules addressing the problem of tumour-

cumour variability and reducing the likelihood of tumour escape due to

antigen loss. Ang88266 to AAG88210 invention.
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cellular immune responses for the prevention and treatment of cancer
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                                            KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
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tumors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELTYLPTNASLSFLØDIOEVQGYYLJAHNOVROVPLORLR IVRGTOLFEDNYALAVLDNG
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                                                                                                                                                                                                                                                                    Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1255;
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98.0%; Score 6709; D
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1240; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Example 13; Page 95-107; 116pp; English
                                              15-SEP-2000; 2000US-0663834
12-SEP-2001; 2001WO-US28572
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                                                                                                                                             Cowsert
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                                                                                               PHARM
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61 ELTYLPTNASLSFLQDIQEVQGYVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                                                                                          N-PSDB; AAD32743
  21-FEB-2002
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/note= "Naturally processed HLA-B44-restricted epitope"
                                                            LESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
                                                                                                                                                                                                                                                 KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP
                               QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE
                                                                                           KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMA
                                                                                                                                                        KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA
                                                                                                                                                                                                          VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLE
                                                                                                                                                                                                                    DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEA
                                                                                                                                                                                                                                                                      PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP
                                                                                                                                                                                                                                                                                                     LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA
                                                                                                                                                                                                                                                                                                             1197 VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
                                                                                                                                                                                                                                                                                                                                          LTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Her-2/Neu protein; immune response; gene therapy; breast
human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAE20479 standard; Protein; 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Her-2/neu protein.
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of numan malignancies, for stimulating and/or expanding T cells specific for human malignancies, for stimulating and/or expanding T cells specific for human malignancies, for stimulating and/or expanding T cells specific for human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the chuman patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in composition or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human Her-2/neu protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated Her-2/Neu polypeptide composition useful for t
prevention and diagnosis of cancer, preferably breast cancer
                                                                                                                                                                                                                                                                                                               Kalos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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98.0%; Pred. No. 0;
ive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 114-117; 129pp; English.
                                                                                                                                                                                                                                                                                                           Foy TM,
                                                                                                                                                                                                                                                                                                       Hand-zimmermann S, Cheever MA,
Mcneill PD, Vedvick TS;
                                                                       14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
14-AUG-2001; 2001WO-US41733
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Best Local Similarity 98.0°
Matches 1240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-280758/32.
                                                                                                                                                                                                                        (CORI-) CORIXA CORP
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The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to BGFR. Its overexpression correlates with a poor prognosis in breast and orexpression correlates with a poor prognosis in breast and orexinan cancers. The invention provides Her-2/neu fusion proteins or nucleic acid molecules. In proteins, mucleic acid molecules. In protein is fused to a Her-2/neu intracellular domain of a Her-2/neu protein is the protein or allocated or enhanced by administering the fusion protein is elicited or enhanced by transfecting cells of an animal ex vivo with a nucleic acid and isolated specific T-cells are useful for inhibiting the transfected cells of contraction or the protein is elicited or enhanced by transfecting cells are useful for inhibiting the transfected cells of an animal ex vivo with a nucleic acid or encoding the fusion protein; and delivering the transfected cells of an animal experient or the animal. The fusion proteins in the form of a vaccine of a protein animal contains the development of a protein and delivering the development of a protein and delivering the development of a protein animal contains and isolated animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eliciting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
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Her-2/neu; oncogene; cancer; tumour; vaccine; human; pl85; tyrosine kinase; receptor; c-erbB2; gene therapy.
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                                                                                                                                                                         /note= "phosphorylation domain"
                                                                                                                     676..1255
/note= "intracellular domain"
990..1255
                                                                                                           /note= "extracellular domain"
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; Pred. No. 0;
7; Mismatches
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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98.0%;
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Best Local Similarity 98.0
Matches 1240; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorylation domain
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                                                 Homo sapiens
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351 REVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYL 410
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                                                                                            NTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVN
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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28-SEP-2000; 2000US-0675904.
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12	Db 1131 LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGA 1190	RESULT 15 AAR39568 ID AAR39568 standard; Protein; 1433 AA. XX AC AAR39568; XX DT 07-FEB-1994 (first entry) XX	DE Sequence of c-erbB-2 tumour antigen. XX XW Tumour antigen; c-erbB-2; glycoprotein. XX XX XX NX NW09316185-A.	19-AUG-1 05-FEB-1 06-FEB-1	PA (CREA-) CREATIVE BIOMOLECULES INC. XX PI Houston LL, Huston JS, Oppermann H, Ring DB; XX DR WPI; 1993-272889/34.	PT New single chain Fv polypeptide binding to C-exbB-2 tumour PT antigen - for imaging or treating breast or ovarian cancer etc. XX PS Disclosure; pages 48-54; 87pp; English. XX		Query Match Query Match Best Local Similarity 97.3%; Pred. No. 0; Matches 1233; Conservative 9; Mismatches 9; Indels 14; Gaps 3; Qy 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60	61 61	Qy 121 DPLANTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDFNNFTV 177 Db 121 DPLANTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIPHKNN 177 Qy 178 SFWLRVPKVSASHLE-NRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGP 236 Db 178QLALTLIDTNRSRACHPCSPMCKGSRCWGESSEHCQSLTRTVCAGGCARCKGP 230
		LPTDCCHEQCAAGCTGERGASDCLACLAFNHSGICELHCPALVTYNTDTFESMFNPEGRYT LPTDCCHEQCAAGCTGFKHSDCLACLAFNHSGICELHCPALVTYNTDTFESMFNPEGRYT FGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHL L	REVRAVTSANIOEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLOVFETLEEITGYL	NTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVN	KDPFCVARCESGVKPDLSYMFIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEGRASP	LTSIISAVVGILLVVVLGVVFGILIKRROOKIRKYTMRRLLOETELVEPLTPSGAMPNOA OMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE OMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE OMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE	AYWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHYRENRGRLGSQDLLMWCMQIA	LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 956	VYMINAKAWIDSECRPRENSELSERAKUPOREVYLONEDIGPASPLUSTFYRSILE VYMINAVKCWMIDSECRPRENSELSRAMARDPOREVVIQNEDIGPASPLUSTFYRSILE VYMINAVKCWMIDSECRPRENSELSELVSERSRARDPOREVVIQNEDIGPASPLUSTFYRSILE DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHRRRSSSTRSGGGDLTLGLEPSEEEA	PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP

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                                                                                                       1197 VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
                                                 YISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHH
                                                                  NTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVN
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Search completed: July 22, 2003, 08:40:44 Job time : 43.1589 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 22, 2003, 08:25:54 ; Search time 23.0157 Seconds Run on:

(without alignments) 5267.077 Million cell updates/sec

Title:

SEQ4-210-224-14 6827 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		p-106 productor	profein-twosine V	epidermal growth f				>	kinase-related tra	epidermal growth f		protein-tyrosine k		kinase-related tra	protein-tyrosine k	protein-tyrosine k	epidermal growth f		protein let-23 [im	tyrosi	protein-tyrosine k		growth	growth	vrosine			like arow	insulin receptor p
	ID	A24571	148161	TVRTNU	GOHUE	A53183	TVCHLV	A47253	S06142	A36223	JC4387	TVFVLV	TVYUH	S35745	S00727	B44776	TVFVEB	GOFFE	A36325	E88257	S70712	S70713	A45558	A42032	A27131	S13807	S13808	INHUR	T43220	A36080
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de	Query	97.9	•	6.58	4	44.4	44.1	42.6	Θ.	34.2	32.9	25.9	24.9	24.1	24.0	23.8	23.7	22.9	20.8	18.3	•	•	•		13.3	11.8	11.1	٠	9.8	
	Score	6684	5870 5	5866	3054	3030	3009.5	2905.5	2602	2333.5	2248.5	1766.5	1703	1647	1640	1623	1621	1561.5	1422	1251	1251	1171	1142	1041	906.5	806.5	754.5	680	671	671
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insulin receptor p	insulin-like growt	insulin receptor-r	insulin receptor-r	protein-tyrosine k	insulin-like growt	ingulin-like growt	protein-tyrosine k	tyrosine kinase Mp	protein-tyrosine k	insulin receptor -	protein-tyrosine k	insulin receptor -	protein-tyrosine k	protein-tyrosine k	mouse developmenta
A34157	T43212	A36502	B36502	T18534	IGHUR1	A33837	A54092	S49004	S05582	T30346	833596	A56081	A36355	150612	148652
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1372	1607	1300	1268	1477	1367	1371	987	977	1114	1390	1091	2148	976	952	987
9.8	7.6	9.6	9.4	9.4	8.8	8.7	8.7	9.8	9.6	9.8	9.8	9.6	8.6	8.5	8.5
670.5	661	655.5	644	643	604	296	591	589.5	588	588	286	585.5	584.5	583.5	583
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 A24571 profein-turogine kinage (RC 2 7 1 112) orbs2 promiseor _ human
	Process: "Troume Assess to 2.7.1.112) esbbs precussor - numan N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein e C;Species: Homo sapiens (man)
	C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change_11-Jun-1999 C;Accession: A24571; A25491; A44188; B44188; I59509; IS7622
	R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, 1 Nature 319, 230-234, 1986
	A; Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growt A; Reference number: A24571; MUID:86118663; PMID:3003577
	A;Accession: A24571 A;Molecule type: mRNA A:Residues: 1-1755 - VAM>
	A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
	Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985 A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epic
	A;Reference number: A25491; MUID:86016729; PMID:2995967 A;Accession: A25491
	A;Molecule type: DNA A:Residues: 737-1031 <sfm></sfm>
	A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
	R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg Science 210, 1112-1119, 1985
	A; Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chro
	A, Accession: A44188
	A; Molecule type: DNA
	A; Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989
	A;Accession: 844188 A:Molecule type: mRNA
	A;Residues: 1-517, RALL', 522, 'S', 524-654,'V', 656-1169,'A', 1171-1255 <cou2></cou2>
	A;Cross-references: GB:M11730; NID:g183986 R:King. C.R.: Kraus. M.H.: Aaronson. S.A.
	Science 229, 94-976, 1985
	A;itte: Ampillication of a novel v-erb8-related gene in a human mammary carcinoma. A;Reference number: IS9509; MUID:85272597; PMID:2992089
	A; Accession: 159509
	A Molecule type: DNA A Molecule type:
	A;Crose-references: GR:1,29396; NID-r459807; DIDN.Abbaseno 1. DID.r460000
	R;Tal, M.; King C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D. Mol Call Riol 7 2507.2601 1007
	Aritle: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptic
	A;Keterence number: I57622; MUID:87286898; PMID:3039351 A;Accession: I57622
	A;Status: translated from GB/EMBL/DDBJ
_	A;Residues: 1-191 <tal></tal>

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EEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDG
                                           1127 YVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFA
         CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
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Keywords: ATP
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86.0%; Score 5870.5; DB 2;
Best Local Similarity 84.9%; Pred. No. 2.2e-244;
Matches 1088; Conservative 57; Mismatches 89;
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C;Superfamily: epidermal growth factor receptor; pr
C;Keywords: ATP
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif
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A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Gemetics:
A;Gene: GDB:RBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Marp position: 17421.1-17421.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Marportion: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorotein; phosphorotein; protein-tyrosine kinase erbB2 #status predicted <BT:-
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorotein; protein-tyrosine kinase erbB2 #status predicted <BT:-
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <ATP:-
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <ATP:-
F;22-1255/Domain: EGF receptor extracellular domain repeat <BE:-
F;24-653/Domain: EGF receptor extracellular domain repeat <BE:-
F;25-653/Domain: EGF receptor extracellular domain repeat <BE:-
F;35-605/Domain: protein kinase homology <AIM:-
F;35-605/Domain: protein kinase homology <AIM:-
F;718-983/Domain: protein kinase ATP-binding site: carbohydrate (ABN) (covalent) #status predicted F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F;686/Binding site: phosphate (Tyr) (covalent) (by protein kinase Lys #status predicted F;753/Active site: Lys #status predicted F;753/Active site: Lys #status predicted F;753/Active site: Dys #status predicted F
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9
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Pred. No. 3.1e-279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.9%;
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Best Local Similarity 97.6'
Matches 1239; Conservative
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pil85 precursor - golden hamster
C;Species: Mesocricctus auratus (golden hamster)
C;Species: Mesocricctus auratus (golden hamster)
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishiki
Gene 140, 251-255, 1994;vation of the Syrian hamster neu proto-oncogene.
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: 148161; MUID:94193007; PMID:7908275
A;Accession: 148161
A;Molecule type: mRNA
A;Recession: 1254 «RES>
A;Cross-references: GB:D16295; NID:9493236; PIDN:BAA03801.1; PID:g747595
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e: The neu oncogene encodes an epidermal growth factor receptor-related protein
prence number: A24562; MUID:86118662; PMID:3945311
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idues: 1-1260 <BAR>
idues: 1-1260 <BAR>
ui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohr nogenesis 12, 1975-1978, 1991
le: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals i azolyl]formamide or N-methyl-N-nitrosourea.
erence number: A61204; MUID:92035293; PMID:1682063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erfamily: epidermal growth factor receptor; protein kinase homology words: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphosphorylation; duplication; glycoprotein; phosphoprotein; protein-tyrosine kinase new facture stedicted «MAT>
1260/Product: protein-tyrosine kinase new facture predicted «MAT>
680/Domain: transmembrane facture predicted «TMN>
980/Domain: protein kinase homology «KIN»
-739/Region: protein kinase ATP-binding moif
191,263,515,576,648/Binding site: carbohydrate (Asn) (covalent) facture predicted
Active site: Lys facture predicted
Active site: Lys facture predicted
1227,1253/Binding site: phosphate (Tyr) (covalent) facture predicted
                                                                                                  1121 DPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLS 1180
                                                                                                                                        1055 GGGELTLGMEPSGEEPPRSPLAPSEGAGSDVFEGELGMGATKGPQSISPRDLSPLQRYSE 1114
                                                                                                                                                                                                                                          PGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPP 1240
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zises: Rattus norvegicus (Norway rat)
e: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
sesion: A24562; A61204
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coule type: DNA
dues: 637-663, VV, 665-702 <MAS>
: authors translated the codon GCA for residue 25 as Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mann, C.1.; Hung, M.C.; Weinberg, R.A.
3 319, 226-230, 1986
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FWLRVPKVSASHLE-----KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNP | SHIPPIN | SHIPPI
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                                                                                                   290 EGRYTFGASCVTTCPYNYLSTEVGSCTLVCPPNNQEVTAEDGTQRCEKCSKPCARVCYGL
                                                                                                                                                                                    ALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE-CVGEGLACHQLCARGHCWGPG
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                                                                                EGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGL
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Nature 309, 418-45, 1984

Altie: Human epidermal growth factor receptor cDNA sequence and aberrant expression Afrite: Human epidermal growth factor receptor cDNA sequence and aberrant expression Afrecession: Monostal Afrecession: MOGS41

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Afrecession: MOGS41

Afrecession: MOGS42

Af
epidermal growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: Nov-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999 C;Date: 15-Nov-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999 C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143; R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J
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K;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley,
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093780
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A; Molecule type: mRNA

A; Rebert W; Gill, G.N.; Speiss, J.

Science 224, 294-297, 1984

A; Reference number: A05281; MUID:84172183; PM;

A; Molecule type: protein

A; Residues: 25-30, 'S', 32-51;454-467 < WEB>
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Nature 309, 418-425, 1984
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Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house)

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                  AWPENRTDLHAFENLEIIRGRIKQHGQFSLAVVSLNITSLGLRSLKEISDGDVIISGNKN 468
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                                                                                                                                        PFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS
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A;Residues: 1-1210 <LUE>
A;Cross-references: GB:U03425
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R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J Biol. Chem. 260, 5205-5209, 1985
A;Title: Identification of residues in the nucleotide binding site of the epidermal grow A;Reference number: A60143; MUID:85182650; PMID:298580
A;Accession: A60143
A;Molecule type: protein
A;Residues: 740-744, X',746-747 cRUS>
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature: 309, 270-273, 1984
A;Title: AfP-stimulated interaction between epidermal growth factor receptor and superco A;Reference number: A38023; MUID:84191554; PMID:6325948
A;Title: AfP-stimulated interaction between epidermal growth factor receptor and superco A;Reference number: A38023; MUID:84191554; PMID:6325948
A;Cohentens: annocation; receptor fard other tyrosine kinases) can nick double-stranded DNA R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J. Cell 59, 33-43, 1989
A;Title: Functional independence of the epidermal growth factor receptor from a domain r A;Reference number: A3331; MUID:90003233; PMID:2790960
A;Comments: annocation; internalization signal
C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor of Comments: Binding of EGF to the receptor leads to internalization of the EGF-receptor of Comments: Binding of EGF to the receptor leads to internalization of the EGF-receptor of Comments: Binding of EGF to the receptor leads to internalization of the EGF-receptor of Comments: Binding of EGF to the receptor leads to internalization of the EGF-receptor of Comments: Binding of EGF to the receptor leads to internalization of the EGF-receptor of the EGF
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C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Superfamily: epidermal growth factor receptor; protein; phosphoprotein; phosphoprotein; supenbroprotein; deficients of Sinasian; signal sequence #status predicted <SIG.
F; 12-4/Domain: signal sequence #status predicted <SIG.
F; 25-645/Domain: EGF receptor #stracellular domain repeat <EE1.>
F; 35-600/Domain: EGF receptor extracellular domain repeat <EE2.>
F; 36-668/Domain: EGF receptor extracellular formain repeat <EE2.>
F; 36-668/Domain: EGF receptor extrac
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F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predic
F;745/Active site: Lys #status experimental
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al Similarity 48.3%; Pred. No. 9.8e-124;
618; Conservative 179; Mismatches 354;
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244 VPKVSASHLEKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRY 295 :	296 TFGASCVTACPYNYLSTDVGSCTLVCPLANQEVTAEDGTQRCEKCSKPCARVCYGLGMEH 355	LREVRAVTSANIQEFACCKKIFGSLAFLPESFDGDPASNTAPLQPEOLOVFETLEEITGY ::::::::::::::::::::::::::::::::::::	LYISAMPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIH	HITHLEFVHTVPWDOLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCV :	536 NCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAH 595	596 YKDPPFCVARCPSGVKPDLSYMPIWKPPDEEGACQPCPINCTHSCVDLDDKGCPAEQRAS 655	656 PLTSIVSAVVGILLVVVLGVVFGI-LIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPN 714	715 QAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEIL 774 	775 DEAYUMAGYGSPYVSRLLGICLTSTYQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ 834	835 IAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKW 894 	895 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT 954	955 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIO-NEDLGPASPLDSTFYRS 1013 	1014 LLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHRRRSSSTRSGGGDLTLGLEPSE 1073	1074 EBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETD 1131	1132 GYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVF 1191 :::	1192 AFGGAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQDPP 1234	1235 ERGAPPSTFKGTPTAENPEYLGLDVP 1260 :
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R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B. Oncogene 6, 673-676, 1991 A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding sit A;Reference number: A43818; MUID:91232866; PMID:2030916	A; Molecule type: mRNA A; Residues: 1-714 <avi> A; Cross-references: GB:X59698</avi>	R;Eisinger, D.P.; Serrero, G. submitted to the EMBL Data Library, June 1992 A;Reference number: S24942 A;Accession: S24942	A;Molecule type: mRNA A;Residues: 969-971, K', 973-1115, 'D' <eis> A;Cross-references: EMBL:Z12608 R:Heisermann, G.J.: Gill. G.N.</eis>	J. Biol. Chem. 263, 13152-13158, 1988 A,Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in A,Reference number: A28941; MUID:88330814; PMID:3138233 A,Accession: A28941	A;Molecule type: protein A;Residues: 689-684, X', 696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009, R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S. submitted to the EMBL Data Library, April 1994	A, Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor A, Reference number: \$45325 A, Accession: \$45325 A, Accession: \$45325 A, Status; preliminary	A; Molecule type: DNA A; Residues: 1-971; 'K', 973-1210 < VER> A; Cross-references: EMBL:X78987; NID:9488830; PIDN:CAASSS87.1; PID:9488831 R; Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.	Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993 A;Title: Expression of the epidermal growth factor receptor gene is regulated in mouse by A;Reference number: 149643; MUID:93126380; PMID:7678348 A;Accession: 149643 A;Accession: 149643	A; Molecule type: mRNA A; Residues: 12-20,22-132 <res> A; Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201</res>	Cydenerics: A;Gene: EGFR C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphopro	F;720-728/Domain: transmembrane #status predicted <tmm> F;648-670/Domain: transmembrane #status predicted <tmm> F;712-977/Domain: protein kinase homology <kin> F;720-728/Region: protein kinase ATP-binding motif</kin></tmm></tmm>	r.oov.oz.) Entating site: phosphate (Ser) (Covalent) #status experimental F:697,1070,1071/Binding site: phosphate (Ser) (Covalent) #status experimental F:993/Binding site: (or 997) phosphate (Ser) (Covalent) #status experimental F:1028/Binding site: (or 1030 or 1032) phosphate (Ser) (Covalent) #status experimental F:1197/Binding site: (or phosphate (Tvr) (Covalent) #status experimental	Query Match Best Local Similarity 48.3%; Pred. No. 1e-122; Length 1210; Matches 621; Conservative 171; Mismatches 362; Indels 132; Gaps 25;	11 LLEALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN 68	69 ASLSFLODIQEVQCYVLIAHNQVRQVFQRLRIVGTQLFEDNYALAVLDNGDFLNNTTP	OY 129 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI 184	SFWLR 24

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R.Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.; Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HER4/p180exbB4, a fourth member of the epiderm
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Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
Accession: A47253
TQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEAD
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                                                                                    ITGYLY ISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGL
                                                                                                                                                                                                    ALIHHNTHLCFVHTVPWDQLPRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGP
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                                             epidermal growth factor receptor precursor - chicken
N-Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C.Species: Gallus gallus (chicken)
C.Species: Callus (chicken)
C.Species: Callus (chicken)
M. 1970-1978, 1988
A.FREference number: A27720; MUD:88261272; PMID:3260329
A.RCCESSION: A.RCCESSION: A.RCCESSION (Chicken)
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A.Residues: 585-1223 «NIL»
A.Cenetics:
A.Genetics:
A.Gen
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47.3%; Pred. No. 8e-122;
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                                                                                                                                                                                                                                                                                                                              68 IEHNRDLSFLRSVREVTGYVLVALNQFRYLPLENLRIIRGTKLYEDRYALAIFLNYRKDG
                                                                                                                                                                                                                                                                                                                                                                      NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                              179 STNGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPY-----VS----
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                          A.Accession: A47253
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: nucleic acid
A.Molecule type: nucleic acid
A.Residues: 1-1308 «PLO»
A.Cross-references: GB:L07868; NID:g337359; PIDN:AAB59446.1; PID:g337360
A.Note: sequence extracted from NCBI backbone (NCBIP:126842)
C.Superfamily: epidermal growth factor receptor; protein kinase homology
C.Keywords: ATP; growth factor receptor
F:716-981/Domain: protein kinase homology «KIN»
F:724-732/Region: protein kinase ATP-binding motif
                                                                                                                                                                                             DB 2; Length 1308;
                                                                                                                                                                                          42.6%; Score 2905.5; DB 2; Length llarity 44.7%; Pred. No. 2.4e-117; Conservative 181; Mismatches 376; Indels
                PMID:8383326
A;Reference number: A47253; MUID:93189574;
A;Accession: A47253
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A;Accession: S06142
A;Molecule type: DNA
A;Redues: 1-1166 (WIT)
A;Cossion: Si0142
A;Molecule type: DNA
A;References: EMBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291
B;Adam, D.; Maeueler, W.; Schartl, M.
Oncogene 6, 73-80, 1991
A;Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphop?
A;Reference number: S13807; MUID:91125882; PMID:1846957
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000 C;Accession: S06142; S13809
R;Witchrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, A.; Robé Nature 341, 415-421, 1989
A;Tile: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu A;Reference number: S06142; MUID:9001S140; PMID:2797166
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A,Gene: mrk
A,Map position: Y
A,Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C,Superfamily: epidermal growth factor receptor; protein kinase homology
C,Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein;
C,Stoperfamin: signal sequence #status predicted <SIG>
F;6-1166/Product: kinase-related transforming protein (Tu) #status predicted <MAT>
E;707-972/Domain: protein kinase homology <KIN>
F;715-723/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                           KGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNED-LG 1001
                                                                                                                                                                                                                                                                                                       1002 PASPLOSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1061
                                                                                  942
                            874
935 KGERLPQPPICTIDVYWWWKKCWMIDADSRPKFKELAAEFSRWARDPQRYLVIQGDDRWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    883 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
                                                                                                                 1062 GGDLTLGLEPSEEEAPRS--------PLAP-SEGAGSDVF
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A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
C;Genetics:
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A;Molecule type: DNA
A;Residues: 821-1025,'N',1027-1098,'A',1100-1
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Length 1166;

Score 2602; DB 1; Pred. No. 2.2e-104;

38.1**%**; 44.5**%**;

Query Match Best Local Similarity

22 12:39:50 2003

Tue Jul

C;Species: Homo sapiens (mān)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C;Dates: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C;Accession: A356223; IS916
R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermé
A;Reference number: A36223; MUID:90083234; PMID:2687875 A;Gene: GDB:ERBB3; HER3
A;Cross-references: GDB:119880; OMIM:190151
A;Cross-references: GDB:119880; OMIM:190151
A;Map position: 12q13-12q13
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Keywords: ATP; phosphotransferase
C;Keywords: ATP; phosphotransferase
F;707-972/Domain: protein Kinase homology <KIN>
F;715-723/Region: protein Kinase ATP-binding motif RiPlowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
A;Title: Molecular cloning and expression of another epidermal growth factor recepton A;Reference number: 159164; MUID:90311312; PMID:2164210 1181 1076 APRSFLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYV 1134 ----- PVRENSITLRNISDPTQNALEKDLDGH- 1055 1056 -----EYVNOPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNT 1106 1182 GKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPS 1241 1107 NONSL---PLVSSGSMDDPDY---QAG-----YQAAF-----LPQTGALTG 1141 34; 68 NASLSFLODIOEVOGYVLIAHNOVROVPLORLRIVRGTOLFEDNYALAVLDNGDPLNNTT 127 128 PVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNOLALTLIDTN 187 126 ----NSSHALRQLRLTQLTEILSGGVYIEKONDKLCHMDTIDWRDIVRDRD----AEIVVKD 178 223 247 VSASHLE-----KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFG 298 188 RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPFNNFTVSFWLRVPK 246 10 GLLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT 67 11 GLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENOYQTLYKLYERCEVVMGNLEIVLTGH 70 1135 APLTCSPQPEYVNQPDVRPQP-----PSPRE-----GPLP-AARPAGATLERAKTLSP kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human Query Match

34.2%; Score 2333.5; DB 2; Length 1342;
Best Local Similarity 39.7%; Pred. No. 8.1e-93;
Matches 526; Conservative 188; Mismatches 460; Indels 151; Gaps A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-559,'G',561-957,'F',959-1063,'G',1065-1342 <RES> A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1, PID:g306841 1142 NGMFLPAAENLEYLG 1156 1242 TFKGTPTAENPEYLG 1256 1020 ---EPCIPPTGH----A,Molecule type: mRNA A,Residues: 1-1342 <KRA> A,Cross-references: GB:M29366 A, Accession: A36223 A, Status: preliminary A; Accession: 159164 C;Genetics: g g ò d ઠે ઠે g 유 q ઠું ઠ ઠે g δ 셤 ò

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1088 PRGCLASESSEGHVTGSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLS 1147
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                      ASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLRE
                                   GVCVASCPHNFV-VDQTSCVRACPPDKMEVD-KNGLKMCEPCGGLCPKACEGTGSG--SR
                                                                  VRAVTSANIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYI
                                                                                340 FQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLNI
                                                                                                                            THLCFVHTVPWDQLFRNPHQALLHTA-NRPEDECYGEGLACHQLCARGHCWGPGPTQCVN
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Cipecies: Rattus norvegicus (Norway rat)
Cipecies: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
Cipecies: 17-Jan-1995
RiHellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
Gene 165, 279-284, 1995
AiTitle: Cloning of the rat ErbB3 cDNA and characterization of the recombinant protes AiTitle: Cloning of the rat ErbB3 cDNA and characterization of the recombinant protes AiTitle cronners: JC4387; MUID:96096535; PMID:8522190
AiReference number: JC4387
AiMolecule type: MRMA
AiResidues: 1-1339 cHEL>
Airesidues: 1
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hor C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hor C;Superfamily: algoral sequence #status predicted < Inc. 19/Domain: signal sequence #status predicted < Inc. 19/Domain: epidermal growth factor homolog #status predicted < MMT>
F;20-1339/Product: epidermal growth factor homolog #status predicted < TMM>
F;640-659/Domain: transmembrane #status predicted < TMM>
F;705-970/Domain: protein kinase homology < KIN>
F;713-721/Region: protein kinase ATP-binding motif
F;339,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosphate (Tyr)
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pidermal growth factor receptor homolog precursor Allernate names: ErbB3 protein; HER3 protein Species: Rattus norvegicus (Norway rat) protein; Date: 17-Jan-1996 #sequence_revision 19-Apr-1996
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                                                                                                                                                                                                                                                                    1220 SPAFDNLYYWDQ------DPPE----RGAPPSTFKGTPTAENPEYLGLDVP 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1117 RYSEDPTVPLPSET - - DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE
                                                                                                                                                                                GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDL
                                                                                                                                                                                                  ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
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                                                                                                                                                                                                                                                    DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
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A;Molecule type: DNA
A;Residues: 1-604 <YAM>
A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 125;
                                                                                                              Length 698;
P;7-59/Product: env protein (fragment) #status predicted <ENV>
F;60-698/Product: protein-tyrosine kinase erbB #status predicted
P;194-459/Domain: protein kinase homology <KIN>
F;202-210/Region: protein kinase ATP-binding motif
F;229/Active site: Lys #status predicted
                                                                                                          Score 1766.5; DB 1;
Pred. No. 8.1e-69;
80; Mismatches 137;
                                                                                                          25.9%; Score 1766.5; 52.2%; Pred. No. 8.1e
                                                                                                     Query Match 25.9%;
Best Local Similarity 52.2%;
Matches 374; Conservative
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C,Superfamily: epidermal growth factor receptor; protein kinase homology
C,Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
F;1-6/Product: gag protein (fragment) #status predicted <GAG>
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N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase
C;Species: avian leukosis virus, ALV
C;Date: 310-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999
C;Accession: B00643; A00643; A00643
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines
Cell 41, 719-726, 1985
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and
A;Reference number: A00643; MUID:85228222; PMID:2988784
A;Accession: B00643
A;Molecule type: mRNA
A;Residues: 1-698 avii.
A;Coss = references: GB:M13881; NID:9211749; PIDN:AAA48763.1; PID:9211750
A;Comment: This protein is synthesized as a gag-env-erbB protein.
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 PAPGQCLSCRNYSREGVCVTHCNFLQGEPREFVHEAQCFSCHPECLPMEGTSTYNGSGSD 571
                                                       ACARCAHFRDGPHCVNSCPHGILG--AKGPIYKYPDAQNECRPCHENCTQGCNGPELQDC
                                                                                                                            DGGKVPIKWMALESILRRRFTHOSDVWSYGVTVWELMTFGAKPYDGIPARRIPDLLEKGE
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                                    OCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSC--VDLDDK
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                                                                                                      GCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEP
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1182 VLGTEEEDED-----EEYEYMNRKRRGSP-PRPP 1209
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                erythroblastosis virus reveals a new type of PMID:6328658
   S.; Martin,
                                                                                                          C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific F;110-395/Domain: protein kinase homology <KIN>
F;138-146/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICTIDUYMIMUKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPSET---DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1183
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   C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule,
                                                                                                                                                                                                                                     IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPARBIPDLLEKGERLPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                                                                                                                         EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                   126;
                                                                                                                                                                            24.9%; Score 1703; DB 1; Length 604; 52.2%; Pred. No. 3.7e-66; ive 76; Mismatches 128; Indels 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Clave Science 224, 1456-1459, 1984
A;Title: Sequencing the erbA gene of avian erythroblastosi A;Reference number: A38022; MUID:84223957; PMID:6328658
A;Accession: A38022
A;Molecule type: DNA
A;Residues: 1-28,'W',30-139,'F',141-145,'V',147-152 < DEB>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1225 NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1254
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Best Local Similarity 52.2'
Matches 360; Conservative
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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C; Species: avian erythroblastosis virus

RESULT 13

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C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specifi F;135-400/Domain: protein kinase homology <KIN> F;143-151/Region: protein kinase ATP-binding motif F;110/Active site: Ly9 #status predicted
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03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997
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54.9%; Pred. No. 8.3e-64;
tive 70; Mismatches 121;
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                                                          Library, March
                                          A;Reference number: S35743
A;Recession: S35745
A;Molecule type: DNA
A;Residues: 1-544 <VEN>
A;Cross-references: EMBL:X12707
C;Genetics:
A;Genetics:
C;Superfamily: enian.
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Matches 345; Conserv
C,Date: 03-Mar-1994 #8
C,Accession: S35745
R,Vennstroem, B.
submitted to the EMBL
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Oncogene Res. 1, 265-278, 1987

A; Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mutant A; Reference number: S00727; MUID:88217326; PMID:2897102

A; Residues: S00727

A; Molecule type: DNA

A; Residues: 1-545 <SCO>
A; Cross-references: EMBL:X06943

C; Genetics:
A; Gene: erbB

C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; phosphotransferase
F:135-400/Domain: protein kinase homology <KIN>
F:143-151/Region: protein kinase ATP-binding motif
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Best Local Similarity 54.9
Matches 345; Conservative
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                                                                                                                                                                                                                                                                                  Gaps
A Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-540 < BRU>
A; Cross-references: GB:X52211
C; Genetics:
A; Gene: erbB
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;130-395/Domain: protein kinase homology < KRN>
F;138-146/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                  90,
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                    23.8%; Score 1623; DB 2;
54.9%; Pred. No. 8.8e-63;
iive 69; Mismatches 120;
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Job time: 31.0157 secs
                                                                                                                                                                                                                                                        Best Local Similarity 54.98
Matches 340; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 22, 2003, 08:12:49; Search time 10.2793 Seconds (without alignments) 5088.033 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

SEQ4-210-224-14 6827 MELAALCRWGLLIALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P04626 homo sapien	ratto	Q60553 mesocricetu	P00533 homo sapien	Q01279 mus musculu	Q15303 homo sapien	rattu	P13388 xiphophorus		Q62799 rattus norv		P00534 avian leuko		avian	-		P70424 mus musculu	P06213 homo sapien		P15127 rattus norv	P15208 mus musculu	P14616 homo sapien	Q25410 lymnaea sta	Q9wtl4 mus musculu		-	P08069 homo sapien	_	P24062 rattus norv	P54760 homo sapien	_	P07949 homo sapien	
SOFFIES	ERB2 HUMAN	ERB2_RAT	ERB2_MESAU	EGFR_HUMAN	EGFR_MOUSE	ERB4_HUMAN	ERB4_RAT	XMRK_XIPMA	ERB3_HUMAN	ERB3_RAT	EGFR_DROME	ERBB_ALV	ERBB_AVIER	ERBB_AVIEU	EGFR_CHICK	LT23_CABEL	ERB2_MOUSE	INSR_HUMAN	ILPR_BRALA	INSR_RAT	INSR_MOUSE	IRR_HUMAN	MIPR_LYMST	IRR_MOUSE	IRR_CAVPO	HTK7_HYDAT	IG1R_HUMAN	IG1R_MOUSE	IG1R_RAT	EPB4 HUMAN	EPA2_MOUSE		INSR_AEDAE
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* Ouery Match	97.9		86.0	44.7		42.6	42.3	38.4	34.3	33.3				23.9	22.1	18.3	•	٠	•	9.8	8	9.7	7.6	•	•	٠	•	•	٠		9.6		9.8
Score	6684	5872	5870.5	3052	3031	2905.5	2886	2618.5	2342.5	2271.5	1883	1749.5	1703	1630	1510	1251	1142.5	678	671	671	670.5	662	661	9	656.5	643	604	S	593.5	S	589.5	288	288
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P29317 homo sapien Q07494 gallus gall	P54761 mus musculu P09208 drosophila	Q00944 gallus gall P09759 rattus norv	Q91738 xenopus lae	PS4762 homo sapien	Q91571 xenopus lae	Q91736 xenopus lae	P34152 mus musculu
EPA2_HUMAN EPB1_CHICK	EPB4 MOUSE INSR DROME	FAK1_CHICK EPB1_RAT	FAK1_XENLA	EPB1_HUMAN	EPBA_XENLA	EPBB XENLA	FAK1_MOUSE
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584.5	583 581	573.5 572.5	569	566.5	564.5	564	563
3.4	36	3 8 8 8	40	4 4 2	43	44	45

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000194; EGFR L domain.

DR InterPro; IPR000195; Euk pkinase.

DR InterPro; IPR000145; FurIn-like.

DR InterPro; IPR00145; FurIn-like.

DR InterPro; IPR004019; VLP motif.

DR Ffam; PF00505; Furin-like; 1.

DR Ffam; PF00757; Furin-like; 1.

DR Ffam; PF00757; VLP; 2.

DR ProDom; PF00701; Euk pkinase; 1.

DR RAMAT; SM00219; TVRC; 1.

DR SWART; SM00219; TVRC; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.

RW Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; KW Transmembrane; Glycoprotein kinase; ATP-binding; Phosphorylation; FT SIGNAL.

TURNORAL.

SIGNAL.

CHAIN. 22 1255 REFFERTOR DOM:
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2
EXTRACELLULAR (POTENTIAL).
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PROTEIN KINASE.
ATP (BY SIMILARITY).
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EMBL; M11761; AAA35808.1; --
EMBL; M11762; AAA35808.1; JOINED.
EMBL; M11763; AAA35808.1; JOINED.
EMBL; M11764; AAA35808.1; JOINED.
EMBL; M11764; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M1706; AAA35808.1; --
EMBL; M1730; AAA75493.1; --
EMBL; X0363; CAA27060.1; --
PIR; A25491; A25491.
PIR; A25491; A25491.
HSSP, P11362; IFGK.
Genew; HGNC: 3430; ERBB2.
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                                                                                                         ILDEAYVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bargmann C.I., Hung M.-C., Weinberg R.A.; "The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth factor receptor-related protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An extended family of protein-tyrosine kinase genes differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Neuroblastoma;
MEDLINE-86118662; PubMed=3945311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
Lai C., Lemke G.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
[3]
STRUCTURE BY NWR OF 650-668.
MEDLINE-92155181; PubMed=1346763;
Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey D.,
Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
"Three dimensional structure of the transmembrane region of the proto-
                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
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Pram; PRO0057; Furin-like; 1.
Pram; PRO1057; Furin-like; 1.
Prodom; PRO0051; Furin-like; 1.
Prodom; PRO00601; Euk_Dkinase; 1.
SWART; SW00261; Ful; 3.
SWART; SW00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
                                                                                                                                                                          oncogenic and oncogenic forms of the neu protein.";
EMBO J. 11:43-48(1992).
-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
ALPHA AND AMPHIREGULIN.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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CYTOPLASMIC (POTENTIAL)
CYS-RICH.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
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HSSP, P11362; 1FGK.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR00174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR00199; XLP motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X03362; CAA27059.1; ALT_INIT
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SIGNAL 1
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KEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLN
                                                           KEILDEAYWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLN
                                                                                                               #CVQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKV
                                                                                                                                                                    PIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOP
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15-DIM-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p188erbB2) (NEU proto-oncogene) (C-erbB-2).
ERBB2 OR NEU.
Besocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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SUBUNIT: HETERODIME
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NCBI_TaxID=10036;
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15-DEC-1998
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BY SIMILARITY.
CHOSPHORYLATION (AUTO-) (IN-LINEED (GLCNAC...) (FR. N-LINKED (GLCNAC...)) (FR. N-LINKED (GLCNAC...) (FR. N-LINKED (GLCNAC...)) (FR. N-LINKED (GLCNAC....)) (FR. N-LINKED (GLCNAC...)) (FR. N-LINKED (GLCNAC....)) (FR. N-LINKED (GLCNAC....)) (FR. N-LINKED (GLCNAC....)) (FR. N-LINKED (GLCNAC.....)) (FR. N-LINKED (GLCNAC.........))
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Pred. No. 3.7e-311;
51; Mismatches 106;
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                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R InterPro; IPR000419; Euk Dkinase.

R InterPro; IPR000119; Euk Dkinase.

R InterPro; IPR001245; Tyr Dkinase.

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R InterPro; IPR00169; YLP_motif.

R Pfam; PF00169; Pkinase; J.

R Pfam; PF00105; Purin-like; J.

R Pfam; PF00107; Pro; J.

R Prodom; P000107; Pkoris J.

R PROSITE; PS00107; PROTEIN KINASE TYR; J.

R PROSITE; PS0011; PROTEIN KINASE DOM; J.

Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;

M Transferase; Tyrosine-protein; Multigene family; Receptor; Signal;

M Transferase; Tyrosine-protein; Multigene family; Receptor; Signal;

M Transferase; Tyrosine-protein; Multigene family; Proto-oncogene; Disease mutation;
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Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
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expression of the amplified gene in A431 epidermoid carcinoma cells.";
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                     GGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSE
                                                                                                   PGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPP
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P00533; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG5; Q92795; O00732;
C006688; Q9BZS2; Q9H225; Q9GZX1; Q9H3C9;
C1-JUL-1986 (Rel. 01, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor protein-tyrosine kinase ErbB-1).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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protein (TEGRS) in ovarian cancer.";
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MEDLINE=21100872; PubMed=11161793;
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TISSUE=Placenta;
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TISSUE=Placenta;
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Mroczkowski B., Mosig G., Cohen S.;
"ATP-stimulated interaction between epidermal growth factor receptor
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BDLINRsB8046483; PubMed=6093780;
Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G., O'Malley B.W.;
Isolation of an evolutionarily conserved epidermal growth factor receptor CDNA from human A431 carcinoma cells.";
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MEDLINE=88217333; PubMed=3329716;
Haley J.D., Whittle N., Bennett P., Kinchington D., Ullrich
Waterfield M.D.;
"The human EGF receptor gene: structure of the 110 kb locus
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"Human and mouse alternative EGFR transcripts encoding only
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BDDILNE=64245835; PubMed=6310563;
Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K.,
Roe B.A., Merlino G.T., Pastan I.;
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Nature 309:806-810(1984)
                                                                                                                                                              sequence analysis and isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          extracellular domain of the receptor.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=85270438; PubMed=2991899;
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                                                                                                                                                           "Comparative genomic se
mouse alternative EGFR
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MEDLINE=98225196; PubMed=9556602;
Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
J. Biol. Chem. 273:11150-11157(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in ovarian cancers.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell DNA synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Rev. Biochem. 56:881-914(1987).

FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                     Sato C., Kim J. H., Abe Y., Saito K., Yokoyama S., Kohda D., "Characterization of the N-oligosaccharides attached to the atypical Asn-X-Cys sequence of recombinant human epidermal growth factor
                                                                                                                                                                                                     MEDLINE=96198132; PubMed=8962717;
Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;
"Analysis of the glycosylation patterns of the extracellular domain
the epidermal growth factor receptor expressed in Chinese hamster
ovary fibroblasts.";
                                                                   Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M., Howk R., Givol D., Ullrich A., Schlessinger J.; All autophosphorylation sites of epidermal growth factor (EGF) receptor and HERZ/new are located in their carboxyl-terminal tails. Identification of a novel site in EGF receptor."; J. Biol. Chem. 264:10667-10671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (shown here), 2/p60/truncated isoform/TEGFR, 3/p110 and 4; are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITES ASN-128; ASN-175; ASN-413; ASN-444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Receptors for epidermal growth factor and other polypeptide
                                                                                                                                                                                                                                                                                                                                       MEDLINE=20193209; PubMed=10731668;
                                                         MEDLINE=89278137; PubMed=2543678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87297456; PubMed=3039909;
                                                                                                                                                                                                                                                                                 Growth Factors 13:121-132(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. 127:65-72(2000)
          Nature 309:270-273(1984)
supercoiled DNA.
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send an email to license@isb-sib.ch).

EMBL; X00588; CAA25240.1; -. EMBL; U95089; AAB53063.1; -. EMBL; U48722; AAC50802.1; -.

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llarity 48.3%; Pred. No. 3.2e-158;
Conservative 178; Mismatches 355;
AAC50804.1; -.
AAC50796.1; -.
AAC50797.1; -.
AAC50798.1; -.
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Matches 618; Conserv
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EMBL; U48725;
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VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLL 1015
                      943 VYMIMVKCMMIDADSRPKFRELIIEFSKMARDPQRYLVIQCDERMHLPSPTDSNFYRALM 1002
                                                                                                                                                                                                               1029 TSRTPLLSSLSATSN--NSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTF 1086
                                                                                                                                                                                                                                                          1134 VAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAF 1193
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STRAIN=BALB/c, and CD-1; TISSUE=Liver, and Decidua;
MEDLINE=93126380; Pubmed=7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
Fariession of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                   EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE
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Genes Dev. 8:399-413(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE FROM N.A.
STRAIN=B6/103; TISSUE=Liver;
MEDLINE=94170986; PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/c; TISSUE=Liver;
BEDLINE=291026370; PubMed=1408137;
Avivi A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            m.
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Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGFR MOUSE STANDARD; PRT; 1210 AA.
001279;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annocation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                          1237 GAPPSTFKGTPTAENPEYL 1255
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STRAIN=BALB/c, TISSUE=Liver;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                            "Comparison of EGF receptor sequences as a guide to study the ligand binding site.", Oncogene 6:673-676\,(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R MGD; MGI:95244; Egfr. L. domain.
R InterPro; IPR000494; EGFR_L. domain.
R InterPro; IPR0001719; Euk_pkinase.
R InterPro; IPR001719; Euk_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR00169; pkinase; I.
R Pfam; PF00169; Ptrin-11ike; I.
R Pfam; PF00107; Prin-11ike; I.
R ProDom; PD000001; Euk_pkinase; I.
R ProDom; PR00107; PR0TEIN_KINASE_ATP; I.
R PROSITE; PS00107; PROTEIN_KINASE_TYR; I.
R PROSITE; PS00101; PROTEIN_KINASE_TYR; I.
R PROSITE; PS00101; PROTEIN_KINASE_DOM; I.
R PROSITE; PS0011; PROTEIN_KINASE_DOM; I.
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EPIDERMAL GROWTH FACTOR RECEPTOR
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EMBL; U03425; AAA17899.1; -.
EMBL; X59684; CAA42219.1; -.
EMBL; L06864; AAA53029.1; -.
EMBL; Z12608; CAA78249.1; -.
HSSP; P11362; 1FGK.
                                                                                                     SEQUENCE OF 969-1117 FROM N.A. STRAIN=C3H;
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SEQUENCE FROM N.A. (ISOFORM JM-A).
TISSUE-Breast carcinoma;
MFDLINE-93189574; Pubmed-833326;
Plowman G.D., Culouscou J.-M., Whitney G.S., Green J.M., Carlton G.W.,
Foy L., Neubauer M.G., Shoyab M.;
"Liggand-specific activation of HER4/p180exbB4, a fourth member of the
 SCONVSRGRECVEKCNILEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAH
                                                                                                                                    :: :| |||||| | :| :: :: AFL------PVPEYVNQ-SVPKRPAGSVQNPVYHNQPLHP------APGRDLHYQN--
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                                                                                          IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRS
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                                               PLTSIVSAVVGILLVVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPN
                                                                                                                        QAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEIL
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2004 (Rel. 41, Last annotation update)
(p180erb84) (Tyrosine kinase erb8-4 precursor (EC 2.7.1.112)
ERB84 OR HER4
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-> W (IN REF. 5)
-> F (IN REF. 4)
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                                                                                                                                                                                                                                                                                                                RECEPTORS (POTENTIAL)

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- ALTERNATIVE FRODUCTS: 2 ISOFORMS; JM-A GROWN HERE) AND JM-B;

ARE PRODUCED BY ALTERNATIVE PROBE ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THER RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THER RESPECTOR: DEAVABLE AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS OF THE HEART.

-1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART, KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROLD, CEREBELLUM, PITUITARY, SPLEEN, TESTIS AND BREAST: LOWER LEVELS IN THYMUS, LING, SALIVARY GLAND, AND PANCREAS.

-1- FTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MIM; 600543; -.

MIM; 600543; -.

MIM; 600543; -.

MIM; 600543; -.

MIM; 600543; -.

MIM; 600543; -.

MIM; 600543; -.

MIREPPO; IPR000149; EGFR L. domain.

InterPro; IPR001214; Furin-like.

R InterPro; IPR001214; Furin-like.

R InterPro; IPR001219; YIP motif.

Pfam; PF00130; PR01869; L. domain; 2.

R Pfam; PF00130; PR01869; L.

R Pfam; PF00130; PR01869; L.

R Probam; PF00177; VLP; Z.

R Probam; PF00177; VLP; Z.

R Probam; PF0019; PR0181M; KINASE TYR; 1.

R PROSITE; PS00107; PR0TEIN KINASE TAP; 1.

R PROSITE; PS00109; PR0TEIN KINASE DOM; 1.

R PROSITE; PS00109; PR0TEIN KINASE DOM; 1.

R PROSITE; PS00101; PR0TEIN KINASE; PROTEIN TINASE RRBB-4.

T TRANSMEM 652 675

DOMAIN 676 1308

CYS. RICH.

T DOMAIN 718 985

PROFIEIN KINASE.
                                                             TISSUE-Fetal brain,
MEDLINE-97476287; PubMed=9334263;
Blenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
Klagsbrun M.;
A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific
tissue distribution and differential processing in response to
phorbol ester.":
J. Biol. Chem. 272:26761-26768 (1997).
-!- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
2, NRG-3, HEPARIN-BINDING ESF-LIKE GROWTH FACTOR, BETACELLUIN AND
NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.
-!- CARTALYTIC ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.
-!- CARTALYTIC ACTIVATED
--- CARTALYTIC ATTRIBUTY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                         tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                                                 SEQUENCE FROM N.A. (ISOFORMS JM-A AND JM-B)
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HSSP; P11362; 1FGK.
Genew; HGNC:3432; ERB4.
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1308 AA; 146807 MW; 5E4AE80985D89761 CRC64;
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ATP (BY SIMILARITY).

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BY SIMILARITY.

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LMSAQTVDSSNIDKFINCTKINGNLIFLVTGIHGDPYNAIEAIDPEKLNVFRTVREITGF
                                   NCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFGPEADQCVACA
                                                                                                                                 SCRRFSRGRICIESCNLYDGEFREFENGSICVECDPQCEKMEDGLLTCHGPGPDNCTKCS
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                                                                    HNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCV
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ERB4_RAT STANDARD; PRT; 1308 AA C 062956; 0922N7; Created)
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1031-1198 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE-Spinal cord;
STRAIN=Sprague-Dawley; TISSUE-Spinal cord;
MEDLINE=97184212; PubMed=903064;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
"Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997)
-!- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.
NOT ACTIVATED BY EGF, GFF-A, AND AMPHREGULIN (BY SIMILARITY).
-!- CATALITIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.

-1- SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBE RECEPTORS (POTENTIAL).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- TISSUB SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND HEART.
                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
Lai C., Lemke G.;
"An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
ERBB4 OR TYRO-2.
                                                                                                                                                                                                                                                      "Neuregulins promote survival and growth of cardiac myocytes. Persistence of ErbB2 and ErbB4 expression in neonatal and adult ventricular myocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
                                                                                                                                                                                                MEDLINE=98221155; Pubmed=9553078;
Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han X.,
Marchionni M.A., Kelly R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESIDUES (BY SIMILARITY).
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InterPro; IPR000719; Buk pkinase.
InterPro; IPR00174; Purin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YuP motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF041838; AAD08899.1; -.
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Pfam; PF00065; pkinase; 1.
Pfam; PF01030; Recep L_domain;
Pfam; PF02757; YLP; Z.
                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 848-901 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U52531; AAC53051.1; -. HSSP; P11362; 1FGK.
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                                                         Rattus norvegicus (Rat).
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                 IISSUE=Heart
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QLALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPFNNF
                               SNWTLVSTIGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPY----
                                                                                                                                                                                       PNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVC
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SMART; SM00261; FU; 4.
SMART; SM00219; TPKK; 1.
SMOSTIE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS010109; PROTEIN KINASE TYR; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Transmembrane; Tyrosine-protein, Multigene family; Phosphorylation.
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44.5%; Pred. No. 3.5e-149;
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PYT -> SYR (IN REF.
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HISPE'S LEGK. L domain.

BR InterPro'; IPR00019; Euk pkinase.

BR InterPro'; IPR002174; Furin-like.

BR InterPro; IPR0022174; Furin-like.

BR InterPro; IPR002250; Ser thr pkinase.

BR PR001545; Tyr_pkinase.

BR PR00159; Pkinase; I.

BR PR00159; Prunin-like; I.

BR PRINTS; PR00109; TYRKINASE;

BR PRINTS; PR00109; TYRKINASE;

BR SMART; SM00219; TYRKINASE;

BR SMART; SM00220; S TKC; I.

BR SMART; SM00220; S TKC; I.

BR PROSTIE; PS00109; PROTEIN KINASE ATP; I.

BROSTIE; PS00109; PROTEIN KINASE DOM; I.

ROSTIE; PS0011; PROTEIN KINASE DOM; I.

R Transmembrane; Glycoprotein; Receptor; Signal; Transferase;

Tyransmembrane; Glycoprotein; Receptor; Signal; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schartl M.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                             Xiphophorus maculatus (Southern platyfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Extinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodonciformes; Poecillidae; Xiphophorus.
                                                                                                                                                                  P13188 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90015140; PubMed=2797166;
Wittbrodt J., Adam D., Malitschek B., Maueler W., Raulf F.,
Talling A., Robertson S.M., Schartl M.;
TNOVEL putative receptor tyrosine kinase encoded by the melanoma-
inducing Tu locus in Xiphophorus.";
Nature 341:415-421(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACT
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SÜBCELLÜLÄR LÖCKTION: TYPE I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                            1231 QDPPERGA--PPSTFKGTPT------AENPEYL 1255
                                                                  1245 HSLPPRSTLQHPDYLQEYSTKYFYKQNGRIRPIVAENPEYL 1285
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PIR; S06142; S06142.
HSSP; P11362; 1FGK.
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EXTRACELLULAR (POTENTIAL)
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                                                                                   PROTEIN KINASE
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NCBI_TaxID=9606;

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PLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYV
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                                                                                      HNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCV
                                                                                                                          STOP STATE S
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbb-3 precursor (EC 2.7.1.112)
(C-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECRETED (SHORT FORM).

-i-ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.
-i-TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
-i-DMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOWAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-i-PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE PBS SUBUNIT OF PHOSPHORYLATION OF THE SECRETED SHILLARITY.
-i-DISBASE: OVEREXERESSED IN A SUBSET OF HUMAN MAWARY TUMORS.
-i-SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                    SEQUENCE FROM N.A. MEDIALS; PubMed=2164210; MEDIATE=9011312; PubMed=2164210; MEDIATE=9011312; PubMed=2164210; Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L., Todaro G.J., Shoyab M.; Molecular cloning and expression of an additional epidermal growth factor receptor-related gene."; Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00261; FU; 3.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
PROSITE; PS50011; PROTEIN KINASE_TOM; 1.
Transmembrane; GlycoproteIn; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
                                                 MEDLINE=90083234; PubMed=2687875; Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.; Traus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.; Isolation and characterization of ERBB3, a third member of ERBB/epidermal growth factor receptor family: evidence for overexpression in a subset of human mammary tumors."; Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
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                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93282822; PubMed=7685162;
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InterPro; IPR00719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; I.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
ProDom; PD000001; Euk pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M29366; AAA35790.1; --
EMBL; M34309; AAA35979.1; --
EMBL; S61953; AAB26935.1; --
PIR; A36223; A56223.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (SHORT TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:3431; ERBB3.
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299 ASCYTACPYNYLSTDVGSCTLVCPLHWGEVTAEDGTQRCEKCSKPCRAVCYGLGMEHLRE 284 GUCVASCPHNYL-VDDTGSCVAACPPDIMED - INGLAWGEPCGGLCFRACEGTGSGSR 284 GUCVASCPHNY-VDDTSCVAACPPDIMED - INGLAWGEPCGGLCFRACEGTGSGSR 3159 WAAVESCPHNY-VDDTSCVAACPPDIMED - INGLASSTRELGSGLALIHHN 419 SAMPDSLPDLSVGTWCTKILLMONDPLITGLANGDPHKILPALDPEKLAVPRTVREITGYLN 1 419 SAMPDSLPDLSVGTWCTKILLMONDPLITGLANGDPHKILPALDPEKLAVPRTVREITGYLN 1 419 SAMPDSLPDLSVGTWCTKILLMONDPLITGLANGDPHKILPALDPEKLAVPRTVREITGYLN 1 419 SAMPDSLPDLSVGTWCTKILLMONDPLITGLANGDPHKILPALDPEKLAVPRTVREITGYLN 1 419 SAMPDSLPDLSVGTWCTKILLMONDLSVGTWCTKILLMONDPHKILPALDPECGGLACHOLCARGFGTGCW 1 419 SAMPDSLPDLSVGTWCTKILLMONDLSVARTWRENGDFGACCWGFGFGGCCGCGGGFGFGCGCCGGGFGFGCGCGCGGGFGGGCGCGGGGGG	127 PSETDGYVA
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rive splicing. 1 132 20 1342 20 1342 20 1342 20 1342 705 1342 705 1342 707 135 1342 707 136 1342 708	NASLSFLODIC NADLSFLOMIN NADLSFLOMIN PVTGASPGCIR NSSHALR RSRACHPCSPW : : NGRSCPPCHEV VSASHLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
SUBCELLULAR LOCATION: TYPE I membrane protein.
SUBCELLULAR LOCATION: TYPE I membrane protein.
DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SDA. OR SH3 DOMAINS OF MAY SIGNAL-TRANSDUCING PROTEINS.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KIRASE.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                        Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 922-1097 FROM N.A.
STRAIN=Spraque-Dawley; TISSUE-Sciatic nerve;
MEDLINE=9718412; PubMed=9030624;
MEDLINE=9718412; PubMed=9030624;
MEDLINE=9718412; PubMed=9030624;

"Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Wallerian degeneration.";

"Neurosci. 17:1642-1659(1997).

-: FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.

-: CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-: SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                                                                                J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00109; PROTEIN_KINASE_TYR, 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
                                                                                                   (EC 2.7.1.112)
                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley, TISSUE=Liver, MEDLINE=96096535, PubMed=8522190, Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland "Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.";
                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                         06279 (062955)
15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-GEOFOCE (Rel. 41, Last annotation update)
(c-erbB3).
              1339 AA
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InterPro; IPR000195; Euk pkinase.
InterPro; IPR001245; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
Pfam; PF00075; Purin-like; I.
Pfam; PF00130; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase; 1.
            PRT;
                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, U29339, AAC28498.2, -.
EMBL, US2530, AAC53050.1, -.
HSSP, P11362, 1FGK.
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SMART; SM00219; TYTKC; 1.
                                                                                                                                                         Rattus norvegicus (Rat).
              STANDARD;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
ERB3_RAT
ID ERB3 RAT
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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPFNNFTV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 SFWLRVPKVSASHLE-----KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                  RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3
EXTRACELLULAR (POTENTIAL).
kinase; ATP-binding; Phosphorylation.
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1122 RPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDGNGYVMPDTHLRGASSSREGTLSSVGLSS 1181
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334 TGSG--SRYQTVDSSNIDGFVNCTKILGNLDFLITGLNVDPWHKIPALDPEKLNVFRTVR 391
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                                         EITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGS
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                                                                                                GLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWG
                                                                                                                                                     PGPTQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEAD
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| 1182 VLGTEEEDED------EYEYMNRKRRGSP-PRPP 1209
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DROME STANDARD; PRT; 1426 AA.

EGFR DROME STANDARD; P81868;
13-64412; 061601; Q9M2G0; P81868;
13-540G-1997 (Rel. 05, Created)
15-DBC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (Egfr)
(Gurken receptor) (Torpedo protein) (Drosophila relative of ERBB)
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RA Admin M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Rederge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beelon K.Y., Enos P.V., Berman B.P., Bhandari D., Bolahakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Lawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dubbin K.J., Bvangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
RA Dubbin K.J., Bvangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
RODIE L., Rodirellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Alalai M., Kalush F., Kazpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalai M., Kalush F., Kazpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalai M., Matuel B., McIntosh T.C., McLeod M.P., McPherson D.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pari V., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM TYPE I), TISSUE SPECIFICITY, AND MUTATION
EGFR OR TOP OR C-ERBB OR DER OR CG10079.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Nooptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS TYPES I AND II).
MEDLINE=94350209; PubMed=8070664;
Clifford R., Schupbach T.;
"Molecular analysis of the Drosophila EGF receptor homolog reveals that several genetically defined classes of alleles cluster in subdomains of the receptor protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lesokhin A.M., Yu S.-Y., Katz J., Baker N.E.;
"Several levela of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila.
Dev. Biol. 205:129-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=85124611; PubMed=2982499;
Livneh E., Glazer L., Segal D., Schlessinger J., Shilo B.-Z.;
"The Drosophila EGF receptor gene homolog: conservation of both
hormone binding and kinase domains.";
Cell 40:599-607(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE SPLICING. STRAIN=Oregon-R; TISSUE=Embryo;
MEDLINE=87002474; Pubmed=3093080;
Schejter E.D., Segal D., Glazer L., Shilo B.-Z.;
"Alternative S, exons and tissue-specific expression of the Drosophila EGF receptor homolog transcripts.";
                                                                                                                                                                                                                                                                                                                                                                         Clifford R., Schupbach T.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM TYPE I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANALYSIS,
MEDLINE=99102120; PubMed=9882502;
                                                                                                                                                                                                                                                                                                      Genetics 137:531-550(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 46:1091-1101(1986).
                                                                                                                  NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ceil #9:13-16(1997).

-!- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS WATGACONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-MAPK PATHMAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.
CRITICAL FOR THE PROLIFERATION OF INAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTREIOR AND DORSO-VENTRAL POLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF PANIOSEROSA AND VENTRAL NEUROSCTODERMAL CELLS, GERM BAND RETRACTION, CELL FATES SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE, UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF TESTIS AND OYARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANALYSIS.
MEDLINE-92018942; PubMed=1936959;
Raz E., Schejter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97248481; PubMed=9094709;
Perrimon N., Perkins L.A.;
"There must be 50 ways to rule the signal: the case of the Drosophila
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spading A.C., Stapleton M., Strong R., Sun E., Sylraskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.Y. Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Nu D., Yang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhong Y.C., Zhan M.D., Yang G., Zhoo Q., Zheng X.H., Zhong F.N., Zhou X., Zhu G., Zho Q., Zheng E.W., Rubin G.M., Venter J.C., "The genome sequence of Env. Rubin G.M., Venter J.C., Spier G. Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                STRAIN=Dackwanrycong;
MEDLINE=85137938; PubMed=2983232;
Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
Madsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
A Drosophila genomic sequence with homology to human epidermal growth factor receptor.";
Nature 314:178-180(1985).
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EMBL; AF052753; AAC08536.1; JOINED.
EMBL; AF052754; AAC08535.1; -.
EMBL; AF052752; AAC08535.1; JOINED.
EMBL; K03054; AAA51462.1; -.
                                                                                                                                                                                                                                                            SEQUENCE OF 959-1078 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPY 307
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                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003494; ARA46732.1; -

BEMBL; X02293; CAA55521.1; -

BEMBL; X78920; CAA55521.1; -

BEMBL; X78920; CAA55521.1; -

BEMBL; X78918; CAA55521.1; -

BEMBL; X7801049; EGFR L domain.

BERFPC; IPR001049; Euk_pkinase.

BILEFPC; IPR00114; Furin-like.

BEAM; PF001030; Recep_L domain; 2.

BEAM; PF001030; Recep_L domain; 2.

BEAM; BR00109; TYRKINASE.

BEAM; BR00109; TYRKINASE.

BEAM; BR00109; PROTEIN KINASE DOM; 1.

BEAMRT; BS00109; PROTEIN KINASE DOM; 1.

BEANSITE; PSS00101; PROTEIN KINASE DOM; 1.

BEROSITE; PSS0011; PROTEIN KINASE DOM; 1.

TYANSIME-protein Kinase; ATP-binding; Signal; Alternative splicing; 3.

TYNOSIME-protein Kinase; ATP-binding; Signal; Alternative splicing; 3.

SIGNAL
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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ATP (BY SIMILARITY).
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EMBL, K03416; AAA50965.1; --
EMBL, K03418; AAA51461.1; --
EMBL, AF109077; AAD26134.1; --
EMBL, AF109078; AAD26132.1; --
EMBL, AF109082; AAD26132.1; --
EMBL, AF109084; AAD26133.1; --
EMBL, AF109084; AAD26133.1; --
EMBL, AF109079; AAD26133.1; --
EMBL, AF109081; AAD26131.1; --
EMBL, AF109083; AAD26131.1; --
EMBL, AF109083; AAD26131.1; --
EMBL, AF109080; AAD26132.1; --
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368 GHLLRDNGACVRSCPQDKMDKGGE-----CVPCNGPCPKTCPGVTVLH------AGNI 414
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                                       368 QEFAGCKKIFGSLAFLPESFDG--DPASNTA-----PLQPEQLQVFETLEEITGYLYIS 419
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                                                    GTHPOFRNLSYFRNLETIHGRQLMESMFAALAIVKSSLYSLEMRNLKQISSGGSVVIQHNR
                                                                                                                                                          OFLRGOECVEECRYLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKD
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                                                                                          AWPDSLPDLSVFQNLQVIRGRILHNGAY-SLTLQGLGISWLGLRSLRELGSGLALIHHNT
                                                                                                                                          HLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWGPGPTQCVNCS
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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SVDNPEYLLNAQTLGVGESPIPTQTIGIPVMGGPGTMEVKVPMPGSEPTSSDHEYYND 1408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.

-!- MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

-!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

25.6%; Score 1749.5; DB 1; Length 634;
Best Local Similarity 52.3%; Pred. No. 6.6e-88;
Matches 370; Conservative 79; Mismatches 135; Indels 123; Gaps
                                                                                                                                                                                 Lyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                            MEDLINE=8522222; PubMed=2988784;
Milsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
Crittenden L.B., Raines M.A., Kung H.-J.;
"c-erbB activation in ALV-induced erythroblastosis: novel RNA
processing and promoter insertion result in expression of an
amino-truncated GGF receptor.";
Cell 41:719-726(1985)
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERMIN PRO0069; DELINASE, INTERNASE, PRO0109; TYRKINASE.
PROD01001; TYRKINASE.
SWART; SM00219; TYRKC; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-profein Kinase; ATP-binding; Oncogene;
                                                                                                                                                                                                                                       Viruses, Retroid viruses, Retroviridae; Alpharetrovirus, NCBI_TaxID=11864;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                         (Rel. 01, Created)
(Rel. 38, Last sequence update)
(Rel. 41, Last annotation update)
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PIR; A00643; TVCHLV.
PIR; B00643; TVFVLV.
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InterPro: DFR000719; Buk pkinase.
InterPro: IPR00145; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
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                                                                                            STANDARD;
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165
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                                                                                                                                                                                                                         Avian leukosis virus.
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                                                                                                                             21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
15-JUN-2002 (Rel.
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                                                                                                                                                                                                                                                                                                                   LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1183
                                                                                                                                                               ----SRTPLLSSLSATSNNSATNCID-----RNGQGHPVREDSFVQRYSSDPTGN 495
NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE 117
                                                                                                             891
                                         118 APNQAHLRILKETEFKKVKVKJCSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANK
                                                                                                            CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                                                      NGVVKDVF------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima K.; "The erbB gene of avian erythroblastosis virus is a member of the src gene family.";
                                                                                I KWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                                                                                                                                                               PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP
                             MPNOAOMRILKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANK
                                                                     EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                                                                                                                                                                                                                                                                                                                                                       Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=79685;
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MEDLINE=84223957; PubMed=6328658;
Debuire B. A. Henry C., Beneissa M., Biserte G., Claverie J.-M.,
Saule S., Martin P., Stehelin D.;
"Sequencing the erbA gene of avian erythroblastosis virus reveals
mer type of oncogene.";
Science 224:1456-1459(1984).
-!-. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrodine-protein kinase transforming protein
                                                                                                                                                                                                                                                                                                                               604 AA
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MEDLINE=84026539; PubMed=6313229;
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P01535;
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LYTOSINE PHOSPHATE.
DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND
ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS
IN CHICKENS.
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                                                                                                      MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE RECEPTOR FOR EPIDERMAL GROWTH FACTOR. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
R -> W (IN REF. 2).
S -> F (IN REF. 2).
I -> V (IN REF. 2).
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InterPro; 1PR000719; Euk_pkinase.
InterPro; 1PR000719; Euk_pkinase.
Pfam; PF00069; pkinase; 1.
SYDOM; D000001; Euk_pkinase; 1.
SWART; SM00119; TyrKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; AT
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EMBL; KO1216; AAA42400.1; -.
PIR; AO0644; TVYUH.
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Matches 360; Conserv
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DOMAIN 11
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1011 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLE 1070
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                                                                                                        59 NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
                                                                                                                                                               653 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                             MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVA I KVLRENTSPKANK
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                                                                                                                                                                                                                                                                                                                                                                                      952 ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF
                                                                                                                                                                                                                                                                                                                                                                                                        593 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEO
                                                  3 CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                                                                                                                                                                        EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 -PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLTAISKLPIDSRYQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 ----SRTPLLSSLSATSNNSATNCIDRNGG-
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   Conservative
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                                                                                       1183
                           PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1125
                                                          495
                                                                                                                                                                --VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLAKTVFE
                                             1126 LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK
                                                                                                                                              1184 NGVVKDVFAF------GGAVENPEYLTPQGGAAPQPHPPPAFSPAFD

    [1]
    SEQUENCE FROM N.A.
    MEDLINE-87064458; PubMed-2878364;
    Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
    "A single amino acid substitution in v-erbB confers a thermolabile phenotype to tsl67 avian erythroblastosis virus-transformed erythroid

 ---NSPST----
                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses, Retroid viruses, Retroviridae, Avian type C retroviruses
                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
V-ERBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Cell. Biol. 6:1751-1759(1986).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M13179; AAA42401.1; -
R PIR; A25231; TVFVEB.
R HISEP: P11862; ITSE.
R HICEPPRO; IPR001245; TYr Dkinase.
R InterPro; IPR001245; TYr Dkinase.
R Pfam; PF00069; Dkinase; 1.
R ProDom; P000001; Euk Dkinase; 1.
R PROSITE; PS00109; PROTEIN KINASE ATP; 1.
R PROSITE; PS00109; PROTEIN KINASE DOM; 1.
R PROSITE; PS0011; PROTEIN KINASE DOM; 1.
R PROSITE; PS0011; PROTEIN KINASE DOM; 1.
R Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
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5B53297AA068B65D CRC64;
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ATP (BY SIMILARITY)
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Pred. No. 1.7e-81;
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418 YRTLMEEEDMEDIVDADEYLVPHQGFF-
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NP BIND 13
BINDING 16
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P11273;
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SEQUENCE FROM N.A.

MEDLINE=88261272; PubMed=3260329;

MEDLINE=88261272; PubMed=3260329;

Lax I., Johnson A., Howk R., Sap J., Bellot F., Winkler M.,

Ullrich A., Vennstrom B., Schlessinger J., Givol D.;

"Chicken epidermal growth factor (EGF) receptor: cDNA cloning,

"Chicken epidermal growth factor alpha.";

"chicken epidermal growth factor alpha.";

transforming growth factor alpha.";

Mol. Cell. Biol. 8:1970-1978(1988)

-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,

AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                             2.7.1.112)
                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC
703 AA
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                                                                                                                         DNA
                                                                                                                         cell
               CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphare.
SUBGELLULAR LOCATION: Type I membrane protein.
MISCELLANGOUS: Banding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cel synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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R InterPro; IPR000494; EGFR L domain.

R InterPro; IPR000494; EGFR L domain.

R InterPro; IPR00129; Euk_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Ffam; PF000757; Furin-like; 1.

R Ffam; PF0007037; Furin-like; 1.

R PROSITE; PS00103; PROTEIN KINASE ATP; PARTIAL.

R PROSITE; PS00103; PROTEIN KINASE DOM; PARTIAL.

R PROSITE; PS00103; PROTEIN KINASE DOM; PARTIAL.

R PROSITE; PS00104; PROTEIN KINASE DOM; PARTIAL.

R PROSITE; PS00104; PROTEIN KINASE DOM; PARTIAL.

R PROSITE; PS00104; PROTEIN KINASE DOM; PARTIAL.

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VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY)
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Pred. No. 7.3e-75;
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    Gaps
    304; Conservative 114; Mismatches 253;
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he : 21.2793 secs
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: July 22, 2003, 08:22:34; Search time 48:5887 Seconds

Without alignments)
5347.444 Million cell updates/sec

Title: SEQ4-210-224-14
Sequence: 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 2000000000

Maximum DB seq length: 2000000000

POSET-processing: Minimum March 100*
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

SPTREMBL 21:*

1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_human:*
5: Sp_human:*
5: Sp_human:*
5: Sp_numan:*
6: Sp_numan:*
7: Sp_numan

Database :

Description		O18735 canis tamil	Q9qx70 rattus norv	O9ep98 mus musculu	O9vh40 xiphophorus	O9w6f6 gallus gall	P79754 fugu rubrin	Ogbihg anonheles a	Oguk79 homo ganien	O8r2x1 mus musculu	086712 avian rous-	086714 avian rous-	O8wvv0 homo sapien	064895 avian ervth	085468 avian ervth	O9wvf5 mus misculu	
SUMMARIES		018/35	1 Q9QX70	1 Q9EP98	3 Q9YH40	3 Q9W6F6	3 P79754	09BIH9	Q9UK79		5 Q86712		OBWYVO	5 Q64895	5 Q85468	L Q9WVF5	1 Q9ERV6
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% Query Match L		7.0	44.8	44.4	38.8	38.5	32.8	28.6	25.7	25.5	25.2	25.2	24.9	24.2	24.1	20.8	20.6
Score	6177	7/70	3057	3028	2652	2631.5	2238	1953.5	1752.5	1739	1720	1718	1697.5	1655.5	1645	1419.5	1403.5
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ALIGNMENTS

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"A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively spliced transcript in normal rat tissue."; Mol. Cell. Biol. 10:2973-2982(1990).
   EEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDG
                                                                                1133 YVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLER-----AKTLSPGKNGVV
                                                                                                                                                        KVAPLICSPQPEYVNQPEVWPQPPLALEGPLPPSRPAGATLERPKTLSPKTLSPGKNGVV
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                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FISHER; TISSUE=LIVER;
A GULTKIGGE K., Dawson T.L., Earp H.S.;
SUDMINGER (NOV-1999) to the EMBL/GenBank/DDBJ databases.
LS SUDMINGER (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; M3734; AAF14008.1; -.
EMBL; M3734; AAF14008.1; -.
HNSP; P11362; IFGK.
R InterPro: IPR000199; EUK PKINASE.
R InterPro: IPR001245; Tyr pkinase.
R InterPro: IPR001245; Tyr pkinase.
R Pfam; PF00757; Furin-like; 1.
R Pfam; PF00757; Furin-like; 1.
R Pfam; PF00105; Pkinase; 1.
R Pfam; PF001009; TyrKINASE.
R PROMOTE; PR00109; TyrKINASE.
R PROMOTE; PR00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00107; PROTEIN KINASE DOM; 1.
R PROSITE; PS00107; PROTEIN KINASE DOM; 1.
R PROSITE; PS00107; PROTEIN KINASE TYP; 1.
R PROSITE; PS00109; PROTEIN KINASE TYP; 1.
R PROSITE; PS00109; PROTEIN KINASE TYP; 1.
R PROSITE; PS00109; PROTEIN KINASE TYP; 1.
R ATP-binding; Receptor; Transferase; Tyrosine-protein kinase.
SEQUENCE 1209 AA; 134891 MW; 96FEE7F6CC1B7773 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
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Pred. No. 2.7e-222;
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Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
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TAENPEYLGLDVPV 1259
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STRAIN=FISHER; TISSUE=LIVER;
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                                                                        MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                           Gaps
                                       28;
     Length 1259;
                                       60; Indels
     DB 6;
 90.4%; Score 6173; D
90.0%; Pred. No. 0;
ive 40; Mismatches
Query Match
Best Local Similarity 90.0°
Matches 1146; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Steter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D., Mainle N.J.;
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"Comparative genomic sequence analysis and isolation of human a
mouse alternative Egfr transcripts encoding truncated receptor
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EMBL; AF275366; AAG28045.1; -
EMBL; AF275364; AAG28045.1; JOINED.
EMBL; AF275365; AAG28045.1; JOINED.
EMBL; AF275365; AAG28045.1; JOINED.
EMBL; AF275367; AAG28045.1; -
HSSP; P11362; IFGK.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor isoform 1.
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InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000199; EUK_pkinase.
InterPro; IPR00179; EUK_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00057; Furin-like; 1.
Pfam; PF00069; Pkinase; 1.
Pfam; PF01030; Recep_L domain; 2.
PRINTS; PR00109; TYRNINASE.
SMART; SM00261; FU; EVKINASE.
SMART; SM00220; STRC; 1.
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1073 1031 1131 1191

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PHSNAVGNPEYLNTAQ-----PTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFP 1178
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LMDEEDMEDVVDADEYLTPQQGFF-------NSPST-----
                                                                   1074 EEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--D
                                                                                                                                                                                                                                  GYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVF
                                                                                                                                                                                                                                                                                                                                                                     1192 AFGGAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----DP-----P
      MALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICT
                                              IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRS
                                                                                                                           LLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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STRAIN=RIO PURIFICATION;
MEDLINE=98241172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock C., Gomez A., D Altschmied J., Schartl M.;
"Activation of the Xmrk proto-oncogene of Xiphophorus overexpression and mutational alterations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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SMART; SM00261; FU; 3.
SMART; SM00219; TYRC: 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequenc
01-JUN-2002 (TrEMBLrel. 21, Last annotat
Receptor tyrosine kinase proto-oncogene.
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HSSP; P1362; 1FGK.
InterPro; IPR0001345; CytC. heme_bind.
InterPro; IPR0001349; EGFR_L. domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR00179; Furin-like.
InterPro; IPR001899; Gram pos anchor.
InterPro; IPR001899; Gram pos anchor.
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PRINTS; PR00109; TYRKINASE
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Pfam; PF01030; Recep L d
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                                                                                                                                                                                    Gaps
                                                                                                                                                                                    Indels 132;
                                                                                                                                              Length 1210;
                                                                                                  62CD021C9DE32E18 CRC64;
                                                                                                                                          tch 44.4%; Score 3028; DB 11; Il Similarity 48.3%; Pred. No. 4.2e-220; 621; Conservative 170; Mismatches 363;
UNKNOWN_1
PROSITE, PS00190, CYTOCHROME C, UNKNOWN : PROSITE; PS00107; PROTEIN KINASE ATP; 1. PROSITE; PS50011; PROTEIN KINASE DOM; 1. PROSITE; PS00109; PROTEIN KINASE TYR; 1. ATP-binding; Receptor; Transferase. SEQUENCE 1210 AA; 134840 MW; 62CD0210
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Duschl J., ά

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ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFY 1011
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PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
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InterPro; PR000494; EGFR L domain.
InterPro; IPR000199; Euk Pkīnase.
InterPro; IPR001199; Furin-like.
InterPro; IPR001149; TuFR c6.
InterPro; IPR004019; TuFP c6.
InterPro; IPR004019; YLP motif.
Pfam; PF00777; Furin-like; 1.
Pfam; PF00077; Furin-like; 1.
Pfam; PF00109; Recept L domain; 1.
Pfam; PF00109; Recept L domain; 1.
Pfam; PR00109; TuFKINASE.
ProDom; PR000001; Euk pkinase; 1.
SWART; SM00261; FU; 3.
PRODOM; PR000001; Euk pkinase; 1.
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NON TER 1 1 SEQUENCE 1137 AA, 127927 MW;
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TISSUE=HINDBRAIN;
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                                                                                                                                                                                                                                                       VOGNLELTYLPTNASLSFLØDIGEVOGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALA
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                                                                                                                                                                                                                                                                                                                                                       176 NNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPFN
                                                                                                                                                                                                                                                                                                                                                                                                                                286 IXYTFGAACVKECPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPKVCDGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           636 -IVSHSSLAVGLVSGLLITVIVALLIVVLLRRRRIK-RKRTIRRLLQEKELVEPLTPSGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
                                                                                                                                                                                                       --NFTVSFWLRVPKVSASHLEKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEHLREVRAVTSANIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592 ACAHYKOPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 577 KCAHFODGPOCIPRCPHGMLGDGDTL-IWKYADKMGQCQPCHQNCTQGCSGPGLSGCRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLG
                                                                                                                                                   Gaps
                                                                                                                                                Indels 150;
                                                                                                             ; DB 13; Length 1165; 1.2e-191;
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SEQUENCE 1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                                                                                                                              38.8%; Score 2652; 44.9%; Pred. No. 1.
                                                                                                                            Similarity
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                                                                    RSILEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEP
                                                                                                                                                                                                                                                                                                                                                            1178 TLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERG
                                                                                                                                                                                                                                                                                                                                                                                          DGYVAPLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAK
                                                                                                                                                                                                                                                                                                            DGH-----EYVNOPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPE
| :: : | |
-----RYKRIN-RQGS-----
                                                                                                                                                               SEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSET
                                                                                                                                                                                                                 ------PVRENSIALRYISDPTQNALEKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 1137;
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Dixon M., Lumaden A.;
"Distribution of neuregulin-1 (nrg1) and erbB4 transcripts
embryonic chick hindbrain.";
embryonic chick hindbrain.";
EMBL; AF121963; AAD31764.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1990 (TrEMBLrel. 21, Last annotation update)
Receptor tyrosine kinase (Fragment).
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1101

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997 PVEENPFVSRRKNGDLQAVDNPEYHN-----APNGQPKAEDEYVNEPLYLNTFANTLE 1049
                                             1050 NAEYL------KONLPEKAKKAPDNPDYWNHSLPPRSTLQHPDYLQEYSTKYFYKONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQFNGERGVCH---KSC-GNYCWGPGKDQCQILTKTVCAPQCNDRCFGTSPRDCCHIECA
                          NPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGA--PPSTFKGTPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 WGLLLALLPP--GAASTQ----VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 WRLILMCVASRLRAASSQTQEAVCPGTQNGLSSTGSQENQYNLNKDRYKGCEIIMGNLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----YPKDG--PSGLNQLGLMNLTEILDGGVQIINNKYLRYGPWVYWRDII-RNNDAPIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DIDCFACRLFNDSGACVPQCPQTLIYNKQT
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                                                                                                                                                                                                                                                                Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryygii, Meopterygii; Taleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                              Fugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1328;
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                                                                                                                                                                                                                                                                                                                                                                                              Gellner K., Brenner S.; "Analysis of 148 kb of genomic DNA around the wnt1 locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ErbB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1328 AA; 148613 MW; A333039258B647E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.8%; Score 2238; DB 13; Best Local Similarity 39.3%; Pred. No. 3.1e-160; Matches 515; Conservative 153; Mismatches 411;
                                                                                                                                                                                   $
                                                                                                                                                                                   1328
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SMART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP;
PROSITE; PS50011; PROTEIN KINASE DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 9:251-258 (1999).

EMBI: AP056116; AAC34391.1; -
HSSP; P11362; 1FGK.
INTERPO: IPR000494; EGFR L. domain.
INTERPO: IPR000199; EMK pkinase.
INTERPO: IPR00174; FurIn-like.
INTERPO: IPR001245; Tyr_pkinase.
Pfam; PF00069; Pkinase; I.
Pfam; PF00069; pkinase; I.
Pfam; PF00069; pkinase; I.
Propom; PF000001; Euk_pkinase; I.
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99177347; PubMed=10077531;
                                                                                   -----AENPEYL 1255
                                                                                                    |||||||
1102 RIRPIVAENPEYL 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Transferase
SEQUENCE 1328 AA; 148
                                                                                                                                                                                   PRELIMINARY;
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              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     979 VSEFSRMARDPQRFVVIQNED-LGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQFF 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRS--PLAP-SEGAGSDVFDG 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVN 1147
                                         220
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                                                                                                                                                                                                                            226 YHTIAAINPEKLNIFQTVREITGYLNIQSWPENMTDFRVFSNLVTIGGRALYSGLSLLIL
                                                                                                                                                                                                                                                                                                                                         286 KQQGITSLQFQSLKQISAGNIYITDNSNLCYYHTVNWTSLFSTPSQKTVIHRNKKAENCT
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                                         LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC
                                                                                                                                                      LHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAE
                                                                                                                                                                               108 TOCPOTFVYNPTTFOLEHWHNAKYTYGAFCVKKCPHNFV-VDSSSCVRACPSSKMEV-EE
                                                                                                                                                                                                                                                                                                                                                                                                346 ADGMVCNELCSSDGCMGPGPDQCLSCKRFIRGRTCIESCNLYDGEFREFANGSVCMECDP
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                                                          QGLG1SWLGLRSLRELGSGLAL1HHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECV
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              Gaps
              66
              Indels
ed. No. 4e-190;
Mismatches 355;
 Pred. No.
              533; Conservative 166;
 46.2%;
 Best Local Similarity
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                                                        501 DSGCWGPGPDQCLSCRNYSRHGTCVAGCHFNSGIPREFAGLNGVCVACHPECKPQTGKAS
                                                                                                                                                                                                                                        HVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQR-CEKCSKP
                                                                                       OVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRS
                                                                                                                                    LRELGSGLALIHHNTHLCFVHTVPWDQLFRNPH-QALLHTANRPEDECVGEGLACHQLCA
                                                                                                                                                                               RGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYVNARH-CLPCHPECQPQNGSVT
                                                                                                                                                                                                                          CFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCV
                                                                                                                                                                                                                                                                        642 DLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVP-----GILIKRRQQKIRKYTMR
                                                                                                                                                                                                                                                                                             GPGLNDC---LEAARLTISSGQITGIALGVPAGLIFCLVLFFLGMLYHRGLAIRRKRAMR
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                                                                                                                                                                                                                                                                                                                     RLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKI
                                           CARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQL
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1433 AA

PRT;

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Q9ВІН9 Q9ВІН9;

RESULT 7 Q9BIH9 ID Q9E AC Q9E

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316 YKDCTIIEGSLEILDQSFDGFQQVYTNFSFGPRYIKIDPDRLEVFSTVKEITGFINIQAH 375
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                                                                                                                                                                Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, expression and localisation of the Anopheles gepidermal growth factor receptor."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ301655; CAC35008.1; -...
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment)
EGFR.
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1433 AA; 159585 MW; E3D9D88967724F07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000195; CytC heme bind.
InterPro; IPR000195; EGFR L domain.
InterPro; IPR000194; EGFR L domain.
InterPro; IPR001719; Euk_Dyfnase.
InterPro; IPR001219; Ser_thr_pkinase.
InterPro; IPR001295; Tyr_pkinase.
InterPro; IPR001295; Tyr_pkinase.
Fam; Pr00105; Furin-like; 1.
Ffam; Pr00105; Furin-like; 1.
Ffam; Pr01030; Recep_L domain; 2.
Fr0Dom; Pr000001; Euk_pkinase; 1.
Fr0Dom; Pr000001; Euk_pkinase; 1.
Fr0Dom; Pr000001; Euk_pkinase; 1.
Fr0Dom; Pr000109; TyrKC; 1.
SWART; SW00120; TYFC; 1.
FR0SITE; PS00119; PROTEIN KINASE_DOM; 1.
FR0SITE; PS00110; PROTEIN KINASE_TYF; 1.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-SUA;
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NON TER
SEQUENCE
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PDSLPDLSVFQNLQVIRGRILHNGAY-SLTLQGLGISWLGLRSLRELGSGLALIHHNTHL
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                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99415551; PubMed=10485918;
Doberty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER-2/nu receptor tyrosine kinase gene encodes a secreted autoinhibitor.";
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner W.i.
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF17761; AAD56009.2; ...
EMBL, AF177761; AAD56009.2; ...
InterPro; IPR000494; EGRR L. domain.
InterPro; IPR00137; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01035, Recep L. domain; 1.
SMART; SM00261; FU; A 45472 MW; FECIBE34752D030C CRC64;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
NCBI_TaxID=9606,
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
                                      Last sequence update)
Last annotation update)
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83.1%; Pred. No. 3.2e-124;
Live 6; Mismatches 34;
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity 83.1<sup>1</sup>
Matches 339; Conservative
PRELIMINARY;
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         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE=94203659; PubMed=8152791;

WEDLINE=94203659; PubMed=8152791;

Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V
Johnsson A., Beug H.;

"Retroviral capture of c-erbB proto-oncogene sequences: rapid
"Retroviral capture of c-erbB proto-oncogene sequences: rapid
evolution of distinct viral genomes carrying mutant v-erbB genes
different transforming capacities.";
Oncogene 9:1307-1320(1994).
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                                                                                                                                       Length 367;
                                                                                                                                                              33; Indels
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
VCBI_TaxID=11950;
                                                                              the EMBL/GenBank/DDBJ databases
                                                                 Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC027080; AAA127080.1; -.
Hypochetical protain John AA127080; SEQUENCE 367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;
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Last annotation update)
                                                                                                                                   Query Match 25.5%; Score 1739; DB 11; Best Local Similarity 88.0%; Pred. No. 2.7e-123; Matches 323; Conservative 11; Mismatches 33;
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InterPro; IPR004028; Retro M.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
Pfam; PF02813; Retro M; I.
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Q86712;
01-NOV-1996 (TFEMBLFEL. 01
01-NOV-1996 (TFEMBLFEL. 01
01-NAR-2002 (TFEMBLFEL. 20
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HSSP; P03322; 1A6S.
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 musculus (Mouse)
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                                                       SEQUENCE FROM N.A.
                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               934 AREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFV 993
                                                                                                                                                                                                                                                                NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM
                                                                                                                                                                                                                                                                                                                                           I PVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         575 PQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
                                                                                                                                                                                                                                                                                                                                                                                                        RRILLOETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       599 -NSPST-----SRTPLLSSLSATSNNSATNCID-----RNGQGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AFGGAVENPEYL 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=94203659; PubMed=8152791;
Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.2%; Score 1720; DB 15; Length 729; llarity 54.8%; Pred. No. 2.1e-121; Conservative 75; Mismatches 118; Indels 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632 PVREDSFVQRYSSDPTGNFLEESIDDGFL-----PAPEYVNQ--LMPKKPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avian rous-associated virus type 1.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
VCBI_TaxID=11950;
                SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

ATP-binding; Transferaes; Tyrosine-protein kinase.

SEQUENCE 729 AA; 80649 MW; 84D2F6914EFEID63 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
ProDom; PD000001; Euk_pkinase; 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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V-ERBB.
                                                                                                                                                                             Local Similarity
hes 358; Conserv
                                                                                                                                                                                                                                                                                 141
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                                                                                                                                                          Query Match
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1117 RYSEDPTVPLPSET - DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE 1174
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702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVALKVLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.2%; Score 1718; DB 15; Length 567; 55.4%; Pred. No. 2e-121; Live 73; Mismatches 112; Indels 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sal Similarity 55.4% 357; Conservative
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Best Local S
Matches 357
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PRT;

PRELIMINARY;

QBWYVO QBWYVO; Q8WYV0 ID Q8 AC Q8

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241 APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              955 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1015 LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    895 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1227 YYWD-QDPPER------1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 1697.5; DB 4; Length 412;
                                                                                                                                                                                                                                                                                                                                  Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao Wan D.F., Gu J.R., "Novel human cDNA clones with function of inhibiting cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyowth...

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF318349; AAL53856.1; -..

R InterPro; IPR000719; EUk_pkinase.

R InterPro; IPR000719; EUk_pkinase.

R InterPro; IPR00019; YLP_motif.

Pfam; PF00069; pkinase; 1.

Pfam; PF007061; YLP; 2.

R Probom; PD000001; Euk_pkinase; 1.

R Probom; PS000101; YLK; 1.

R PROSTTE; PS000116; EF HAND; UNKNOWN 1.

R PROSTTE; PS000116; EF HAND; UNKNOWN 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.5e-120;
5; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gag, v-erb-A, v-erb-B protein. GAG, V-ERB-A, V-ERB-B.
Avian erythroblastosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 80.59
Matches 330, Conservative
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Q64895;
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R InterPro; IPR000719; Euk pkinase.

R InterPro; IPR000719; Stdhram receptor.

R InterPro; IPR00145; Tyr pkinase.

R InterPro; IPR001628; Znf_C4steroid.

R Eam; PPF00104; hormone_rec; 1.

R Pfam; PPF00105; zf-C4; 1.

R Pfam; PPF00105; zf-C4; 1.

R PRINTS; PR00139; ZRRDHORMONER.

R PRINTS; PR00001; Euk_pkinase; 1.

R PRODOM; PD000001; Euk_pkinase; 1.

R PRODOM; PD000001; Euk_pkinase; 1.

R PRODOM; PD000019; TyrKc; 1.

SMART; SM0019; TyrKc; 1.

SMART; SM0019; TyrKc; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R ATP-binding; DNA-binding; Nuclear_protein; kinase; 2 ince-finder.
                                                                                                                                                            R.C.
Retroid viruses; Retroviridae; Avian type C retroviruses
                                                                                 Ouery Match 24.2%; Score 1655.5; DB 15; Length 962; Best Local Similarity 39.7%; Pred. No. 2.4e-116; Matches 422; Conservative 109; Mismatches 260; Indels 273;
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RAY SEQUENCE FROM N.A.

RAY MEDLINE=88211326; PubMed=2897102;

RAY MEDLINE=88211326; PubMed=2897102;

RAY Occting P., Vennistrom B., Jansen M., Graf T., Beug H., Haymann M.J.;

RT "Common site of mutation in the erbB gene of avian erythroblastosis

RT virus mutants that are temperature sensitive for transformation.";

RAY Nocesen Free. 1:265-278(1987).

BR HSSP: P1362; 1FGK.

BR HSSP: P1362; 1FGK.

BR HSSP: P1362; 1FGK.

BR InterPro; 1PR001245; Tyr_pkinase.

BR InterPro; 1PR001245; Tyr_pkinase.

BR Probom; P0000001; Buk_pkinase; 1.

BR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

BR PROSITE; PS00107; PROTEIN KINASE TYR; 1.

BR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

BR ROSITE; PS00109; PROTEIN KINASE TYR; 1.

BR ATP-binding; Transferase; Tyrosine-protein kinase.

SEQUENCE 545 AA; 60899 MW; 140DCE8CCA0F8AF4 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-erbB gene.
Viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid virus
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                                                                                                                  58 GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL
                                                                                                                                                                                                                   883 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
                                                                                                                                                                                                                                                                                                                            .062 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ
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                                   GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQOKIRKYTMRRLLQETEL
                                                                                                         VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
                                                                                                                                           ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
                                                                                                                                                                               LGSQDLLNWCMQ1AKGMSYLEDVRLVHRDLAARNVLVKSPNHVK1TDFGLARLLDIDETE
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Alternative Transcripts from the Human and Mouse EGFR Genes Encode Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UTUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                 92;
 Length 545;
                 Indels
DB 15;
                   121;
24.1%; Score 1645; DB 15; 54.9%; Pred. No. 6.5e-116; ive 70; Mismatches 121;
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                 345; Conservative
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          Best Local Similarity
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                              STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Stelter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                               of human a
d receptor
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                                                                                                                                                                                                                                                                                            Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               655 AA; 72906 MW; 6B34063B1BC928CB CRC64;
                                                                                                                                                                                               "Comparative genomic sequence analysis and isolation o mouse alternative Egfr transcripts encoding truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000494; EGFR L domain.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=LIVER;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF124513; AAD44149.1; --
EMBL, AF275366; AAC28047.1; --
EMBL, AF275364; AAC28047.1; JOINED.
EMBL, AF275365; AAC28047.1; JOINED.
EMBL, AK004944; BAB23688.1; --
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Pfam; PF01030; Recep L domain; 2.
SMART: SM00261; FU; 3.
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FROM N.A.
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SEQUENCE
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296 TFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEH 355
    596 YKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC 648
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Search completed: July 22, 2003, 09:00:45 Job time : 54.5887 secs

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July 22, 2003, 08:11:38; Search time 38.1589 Seconds (without alignments) 4403.399 Million cell updates/sec
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| SIDS2/gcgdata/geneseqp_embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqf_embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqf_embl/AA1981.DAT:*
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1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1261
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human herequlin 2	Human tyrosine kin	HER2 transgene pla	Human HER2 (ErbB2)	HER-2/neu protein.	Human HER-2/neu on	Human HER-2/neu pr	Amino acid seguenc	Human HER-2/neu pr	HER2/neu amino aci
SUMMARIES		AAE12130	AAB60167	AAU74545	AAW01111	AAW92406	AAB21198	AAY84780	AAB85458	AAG88267
DB	21	22	22	23	11	20	21	21	22	22
¢ Query e Match Length DB I	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255
& Query Match	98.0	98.0	98.0	98.0	97.9	97.9	97.9	97.9	97.9	97.9
Score	0699	0699	0699	0699	6684	6684	6684	6684	6684	6684
Result No.	-	7	ю	4	S	9	7	80	σ	10

Human Her-2 protei	\sim	Her-2/neu	۳	Sequence of c-erbB	east	Human HER-2/neu pr	ď		Mouse Her-2/neu pr	Amino acid sequenc		Human HER-2/neu fu	Her-2/neu extracel	Mouse Her-2/neu ex	Mouse Her-2/neu ex	Human HER-2/neu fu	Her-2/neu extracel	Her2-GM-CSF immuno	Extracellular HER-	Human Her-2/neu on	Human ErbB2 oncopr		DC8scFv-erbB2EC fu	Ω,			Human protein for	Human protein for	Amino acid sequenc	Human EGF receptor	Her	epide	Amino acid sequenc	epide
AAE24067	AAE2047	AAM51143	AAU7711	AAR39568	AAU9892	AAB2120	AAB2119	AAM5114	AAB2120	AAG62860	·	AAB21203	AAM51148		AAM51153		AAM51149	AAW19764		AAM51145			AAY4499	AAR08222	AAE2048	AAE2048	AAE2048	•	AAB1925	AAY5061	AAE2301	AAM5076	AAB68420	ABP51768
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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign T helper epitopes were identified (see features table). The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
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/label= insertion region
/note= "sultable For foreign epitope insertion"
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins).

(PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APC8) of the animals immune system of: (1) at least 1 B-cell group derived from the PA and/or at least 1 B-cell group derived from the Cell-associated PA; and (2) at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
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ILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWC
          MQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPI
                                                                        SLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPS
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                                     MQI AKGMSYLEDVRLVHRDLAARNVLVKSPNHVKI TDFGLARLLDI DETEYHADGGKVPI
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/note= "Antigenic epitope"
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex. (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as compounts of anti-cancer vaccines and to expand immune effector calls that are specific for cancers characterised by expression of the breast cancer antigen, HBR-2. Polynucleotides that encode peptides of the invention are useful as Pybridisation probes and as primers for the detection of genes of transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HBR-2. Compounds of the invention are designed based on the HBR-2 antigenic peptide
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                                                                                                                                                                   The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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                                                       Treating tumors, particularly breast cancers, receptor and does not respond to an anti-ErbB conjugating the antibody to a maytansinoid -
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N-PSDB; AAF24297.
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     Sliwkowski
                                                                                                                   Example 3; Fig 7; 93pp; English
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Best Local Similarity 97.8
Matches 1241; Conservative
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    Schwall
                            2002-163686/21.
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                                        N-PSDB; ABK14058
    Erickson S,
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                        CTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYR
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                                                                            MOIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPI
                                                                                                                                            KWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU74545 standard; Protein; 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HER2 (ErbB2) polypeptide.
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EYLGLDVPV 1255
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SCHWALL R.
SLIWKOWSKI M.
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(SCHW/)
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ID AAU7
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The invention relates to treating a tumour in a mammal, where the tumour is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, compising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stoomach, endometrium, ally any gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB: The method is also useful for treating neuronal, glial, astrocytal, hypothalmic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, anglogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
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Pred. No. 0;
1; Mismatches 5;
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120 120

180 180 240 232 292 286 352 346

412 406 472 466 532 526 592 586

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GRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLG
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                                                                                                                                                                                         Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The product of everyerssed in various cancers, including breast, overtain, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                     DNA encoding HER-2-new poly:peptide(8) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is associated
                                                                                                                                                                                                                                                                                                                                    Length 1255;
                                                                                                                                                                                                                                                                                                                                                        Indels
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97.9%; Score 6684; DB 17;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1239; Conservative 2; Mismatches 6;
                                                                                                                                                                      Claim 2; Page 56-61; 71pp; English
                        95US-0414417
   96WO-US01689
                                              WASHINGTON
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                                                                                       WPI; 1996-455361/45.
N-PSDB; AAT40739.
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                        31-MAR-1995;
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                               PNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKE
                                                                                                                       CTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYR
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breast cancer; ovary cancer; colon cancer; lung cancer;
prostate cancer; immunisation; tumour; vaccine; vector.
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/label= Intracellular_domain
/note= "claimed domain, useful for
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EYLGLDVPV 1255
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This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                                                                                                                                   immune response
for treating or
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                                                                                                                                                                                                                                                                                                                                   Length 1255;
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                                                                                                                                                Use of HER-2/neu polypeptides - for eliciting an an HER-2/neu associated malignancy, particularly
                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                               Query Match 97.9%; Score 6684; DB Best Local Similarity 97.6%; Pred. No. 0; Matches 1239; Conservative 2; Mismatches
                                                                                                                                                                                          Claim 3; Column 31-38; 26pp; English
              96US-0625101.
93US-0033644.
93US-0106112.
95US-0414417.
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                                                                                          Disis ML;
                                                                                                              WPI; 1999-152835/13.
N-PSDB; AAX01912.
                                                                                                                                                                                                                                                                                                            1255 AA;
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              01-APR-1996;
17-MAR-1993;
12-AUG-1993;
                                                                   VINU ( WINU)
                                             31-MAR-1995;
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                                                        CTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYR
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                                           RASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAM
                                                                                                                                  ILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWC
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/note= "region which elicits immune response"
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malignancy; treatment; tumour.
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The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGCR). It probably plays a part in call growth differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immure response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
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Pred. No. 0;
2; Mismatches
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Best Local Similarity 97.6%;
Matches 1239; Conservative ;
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           CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                             KWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPI
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CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                               RASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAM
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                                                                                                                                                      The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteins residues, compared to the unspliced protein. The erbB-2 polymucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                                                                           Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
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The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as p185 or c-exbB2).
                                                                  New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
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ive 2; Mismatches
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Best Local Similarity 97.6
Matches 1239; Conservative
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cytostatic; vaccine; p185; c-erbB2.
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immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                                                                            PNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKE
                                                                 ILDEAYWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWC
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The present invention described solated prepared HKAZ/new epicopes (I).

Also described are: (1) a clonal cytocoxic T lymphocyte (CTL) that is

Culture in vitro and binds to a complex of an epitope (I), bound to a

CC human leukcoyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)

and a second epitope and the peptide is less than 50 contiguous amino

coids that have 100% identity with a native peptide sequence of HERZ/new;

CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical

cxtipient; (4) an isolated nucleic acid encoding a peptide comprising

(I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic

cxtipient; (4) an isolated nucleic acid encoding (II). (I) has cytostatic

cxtipient; (4) an isolated nucleic acid encoding (II). (I) has cytostatic

cxtipient; (4) an isolated mucleic acid encoding (II). (I) has cytostatic

cxtipient; (5) an isolated mucleic acid encoding (II). (I) has cytostatic

cxtipient; (1) are useful for inducing cellular immune response for the

prevention and treatment of cancer. (I) and (II) are useful for

cxtipient and treatment of cancer. (I) and (II) are useful for

cxtipient and treatment of cancer. (I) and (II) are useful for

cxtipient hen incubated with a T lymphocyte sample form a patient and

cxtipient hen incubated with a T lymphocyte sample form a patient and

cxtipient hen incubated with a T lymphocyte to (I) or (II). Epitope

cxtipient hen incubated of bound T lymphocyte to (I) or (II). Epitope

cxtipient immunogenicity. The possible pathological side effects caused by

cxtipient tumour associated molecules addressing the problem of tumour

cxtipient variability and reducing the likelihood of tumour escape due to

cxtipient loss. AAG88266 to AAG89121 minod of tumour escape due

cxtipient loss. AAG88266 to likelihood of tumour escape due

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                inducing
                                                                                                                    invention describes isolated prepared HER2/neu epitopes (I)
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                                       cancer
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Pred. No. 0;
2; Mismatches 6; Indels 22;
                    for
            An isolated prepared HER2/neu epitope useful in a vaccine f
cellular immune responses for the prevention and treatment
                                                                              English
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                                                                            15; 199pp;
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Matches 1239; Conservative
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LIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPT

of Human tumors

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                        Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1255
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Best Local Similarity 97.6%; Pred. No. 0;
Matches 1239; Conservative 2; Mismatches
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                           12-SEP-2001; 2001WO-US28572
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                                                        15-SEP-2000;
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21-MAR-2002
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                                          CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                          MQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPI
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                                                                                  CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                            RASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAM
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                         QCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVA
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukcoyte antigen (HLA) -B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer, or preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for human malignancies, for selmulating and/or expanding T cells specific for human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the chuman patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centire Her-2/Neu gene or gene fragments of intererst, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human Her-2/neu protein.
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                                                                                                                                                                                                                          Novel isolated Her-2/Neu polypeptide composition useful for oprevention and diagnosis of cancer, preferably breast cancer
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Mcneill PD, Vedvick TS;
                                                        14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
                              14-AUG-2001; 2001WO-US41733
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                                                                                                                (CORI-) CORIXA CORP
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1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
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human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                              CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                        PNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKE
                                                                                                                                                       PNOAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKE
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EYLGLDVPV 1255
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The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and overcing an extracellular domain correlates with a poor prognosis in breast and coverage comprising the fusion proteins or nucleic acid molecules. In protein is fused to a Her-2/neu intracellular domain or protein is fused to a Her-2/neu intracellular domain or protein is fused to a Her-2/neu intracellular domain or protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid and isolated specific T-cells are useful for inhibiting the transfected cells or cancer especially breast, ovarian, colon, lung or prostate cancer in a patient. I cells that specifically react with a Her-2/neu fusion protein, colon, lung or prostate cancer in a patient. I cells that specifically react with a Her-2/neu fusion protein of remove tumour cells from a sample in conding the that specifically react with a Her-2/neu fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQCCQVVQGNL
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Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
tyrosine kinase; receptor; c-erbB2; gene therapy.
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                                                                                                                                                                                  /note= "phosphorylation domain"
                                                                                                                                               /note= "intracellular domain"
990..1255
                                                                                                              /note= "extracellular domain"
676..1255
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                 cocation/Qualifiers
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                                                                                                                                                                                                                                                                                 03-AUG-2001; 2001WO-US24283
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N-PSDB; ABA92250.
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                                                  Homo sapiens
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347 MEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEI 406
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                                                QCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVA
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                               TGYLYISAWPDSLPDLSVPQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLA
                                                                                               LIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPT
                                                                                                                    LI HHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPT
                                                                                                                                                                                  QCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVA
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AAU77114 standard; Protein;
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                                   LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPFNNFTVSF
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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Z)neu or a polymucleotide encoding an immunogenic Annigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic lymphocytic leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-Z)neu polypeptide.
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1127 YVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFA 1186
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ilarity 97.1%; Pred. No. 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 22, 2003, 08:25:54; Search time 23.0157 Seconds Run on:

(without alignments) 5267.077 Million cell updates/sec

Title: Perfect score:

SEQ4-250-264-14 6839 1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1261

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein-tyrosine k	protein-tyrosine k	p-185 precursor -	epidermal growth f			epidermal growth f	>	kinase-related tra	epidermal growth f		protein-tyrosine k		kinase-related tra	protein-tyrosine k		epidermal growth f	epidermal growth f	protein let-23 [im	protein-tyrosine k	protein-tyrosine k	epidermal growth f			-	protein-tyrosine k	insulin-like growt	insulin receptor p	receptor
SUMMARIES	ID	A24571	TVRTNU	148161	GOHUE	A53183	TVCHLV	A47253	S06142	A36223	JC4387	TVFVLV	TVYUH	S35745	S00727	B44776	TVFVEB	GOFFE	A36325	E88257	S70712	870713	A45558	A42032	A27131	S13807	380	T43220	A34157	A36080
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•	Query Match	- 60	86.2	86.0	45.6	45.2	44.9	3	39.1	35.0	33.7	25.8	24.9	24.1	24.0	23.7	23.7	23.4	21.7	18.5	18.5	17.1	ė.	16.1	•	;	÷		10.5	
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A,Status: translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-191 <TAL>

insulin receptor p	insulin-like growt	protein-tyrosine k	insulin receptor-r	insulin receptor-r	ingulin-like growt	insulin-like growt	insulin receptor -	insulin receptor -	insulin receptor (protein-tyrosine k	tyrosine kinase Mp	protein-tyrosine k	protein-tyrogine k	protein-tyrogine k	protein-tyrosine k
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718	691	687	685.5	675	649	635	620	611.5	909	594.5	589.5	588	586	584.5	583.5

ALIGNMENTS

RESULT 1	
protein-tyrosin NyAlternate nar	protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human NiAlternate names: C-erb-B-2 protein precursor; kinase-related transforming protein e
C;Species: Home C;Date: 25-Oct. C:Accession: A	-Cispecies: Homo Bapiens (man) Cibate: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999 CiAccession: A24571: A25401: A44188: R44188: T55809: T57573
R;Yamamoto, T.	R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T Nature 319 230-234 1986
A;Title: Simil. A;Reference nur	A:Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growt A:Reference number: A24571; MUID:86118663; PMID:3003577
A; Molecule type: mRNA	424571 424571 1956 - WAM.
A;Cross-referen	A.Krostauce: 1-1233 (1AT) Krosta - Kreferences (GB:K703363; NID:g31197; PIDN:CAA27060.1; PID:g31198 R.Semba. K.: Kamata N.: Tovochima K.: Vanamoto T.
Proc. Natl. Aca	Proc. Natl. Acad. Sci. U.S.A. 82, 497-6501, 1985 A; Title: A v-erbB-related protooncodene. c-erbB-2, is distinct from the c-erbB-1/epid
A:Reference number:	A;Reference number: A25491; MUID:86016729; PMID:2995967
A; Molecule type: DNA	96: DNA W. 72-1031 A CEM.
A; Cross-referen	A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
R;Coussens, L.	R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg Science 210, 1132-1130, 1085
A,Title: Tyros:	sine kinase receptor with extensive homology to EGF receptor shares chro
A; Reference nur	A44188; MUID:86070181; PMID:2999974
A; Molecule type: DNA	144188 De: DNA
A;Residues: 74(40-910 <coui></coui>
A; Cross-rerences: A:Accession: B44188	ences: GB:M12036; N1D:G183988; PIDN:AAA35978.1; PID:g183989 344188
A; Molecule type: mRNA	oe: mRNA
A:Cross-referen	A;Residues: 1-517, RALL', S22', S', S', S24'-654, V', 656-1169, 'A', 1171-1255 <couz> A;Crose-references GR.M11710, NID.G181864</couz>
R, King, C.R.,	R.King, C.R.; Kraus, M.H.; Aaronson, S.A.
A, Title: Ampli	974-976, 1985 Ification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference nur	IS9509; MUID:85272597; PMID:2992089
A;Accession: 159509 A:Status: translate	AfACCEBION: 1295UY A:Ritis: translated from CB/DMBI/DDD1
A; Molecule type: DNA	pe: DNA
A, Residues: 832-909 <rex></rex>	12-909 <rex></rex>
A;Cross-referer	
Mol. Cell. Bio	Myl. Cell. Biol. 7, 2597-2601, 1987
A; Title: Human	A, litle: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptio
A;Reference number: A:Accession: 157622	umber: I57622; MUID:87286898; PMID:3039351 157622
A;Status: trans	A.Status: translated from GB/EMBL/DDBJ

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C, Accession: 31-uc-11300 #BEQUENCE_revision 31-Dec-11988 #text_change 11-Jun-1999
C, Accession: A24562, A61204
R; Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Rautre 319, 226-230, 1986
A.Title: The neu oncogene encodes an epidermal growth factor receptor-related protein: A, Reference number: A24562, MUID:86118662; PMID:3945311
A, Accession: A24562
A, Molecule type: mRNA
A, Residues: 1-1260 < BAR>
A, Gross references: EMBL:X03362; NID:956745; PIDN:CAA27059.1; PID:956746
B, Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohe Carcinogenesis 12, 1975-1978, 1991
A-Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals n. A. Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals n. A. Title: Direct DNA Sequencing of the rat neu oncogene transmembrane domain reveals n. A. Title: Direct DNA Sequencing of the rat neu oncogene transmembrane domain reveals n. A. Title: Direct DNA Sequencing of the rat neu oncogene transmembrane domain reveals n. A. Title: Data Collection of the collect
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
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                                                                                           LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM
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A, Molecule type: DNA
A, Residues: 637-663, 'V', 665-702 < MAS>
A, NOte: authors translated the codon GCA for residue 25 (2, Genetics: A, Generics: A, 
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                                                                                A Gene: GDB.ERBB2; NGL; NEU; HER-2
A; Cross-references: GDB.120613; OMIM:164870
A; Cross-references: GDB.120613; OMIM:164870
A; Cross-references: GDB.120613; OMIM:164870
A; Cross-references: GDB.120613; OMIM:164870
A; Note: the list of introns is incomplete
C; Function:
A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phospho
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tive 3; Mismatches 12;
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Yamazaki, Y.; Ishika
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C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-034-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Date: 02-5041-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; I.
Gene 140, 251-255, 1994
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: 148161; MUID:94193007; PMID:7908275
A;Accession: 148161
A;Accession: 148161
A;Accession: 148161
A;Accession: 148161
A;Actus preliminary; translated from GB/EMBL/DDBJ
A;Graus: references: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID:g747595
C;Genetics:
A;Gene: neu
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein kinase homology
E;718-993/Domain: protein kinase homology «KIN»
F;726-734/Region: protein kinase ATP-binding metif
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C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication, glycoprotein; phosphoprotein; phosphoprotein; signal sequence #status predicted <SIG>F1-19/F00main: signal sequence #status predicted <SIG>F20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>F; 658-680/Domain: transmembrane #status predicted <TWN>F; 733-988/Domain: protein kinase homology <KIN>F; 731-998/Region: protein kinase ATP-binding motif
F; 711-191, 263, 535, 576, 634/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 759/Active site: Lys #status predicted
F; 758/Active site: Lys #status predicted
F; 882, 1227, 1253/Binding site: phosphate (Tyr) (covalent) #status predicted
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	901 LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI 960
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7	141 PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENP 1200
ਜ	QPEYVNQPEVRPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFTFGGAVEN
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A53183

Cybecides: Mus musculus (house mouse)

Cybecides: Mus musculus (house mouse)

C;Accession: A53183; A43818; E24942; A28941; S45325; I49643

Genes Dev. B, 399-413, 1994

A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor A;Reference number: A53183; MUID:94170986; PMID:8125255

A;Accession: A53183

A;Accession: A53183

A;Residues: 1-1210 cLUE>

A;Cross-references: GB:U03425
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                                                                     A; Accession: A60143
A; Molecule type: protein
A; Residues: 740-744, X; 746-747 < RUS>
A; Molecule type: protein
A; Residues: 740-744, X; 7,746-747 < RUS>
B; Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A; Title: AFF stimulated interaction between epidermal growth factor receptor and supercd
A; Title: AFF stimulated interaction between epidermal growth factor receptor and supercd
A; Contents: annotation; receptor activity
A; Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
A; Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
A; Contents: annotation independence of the epidermal growth factor receptor from a domain x
A; Reference number: A3333; MuID:9000323; PMID:2790960
A; Contents: annotation; internalization signal
C; Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor c
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross references: GDB:120610; OMIM:131550
A;Gross references: GDB:120610; OMIM:131550
A;Gross references: GDB:120610; OMIM:131550
A;Gross references: GDB:120610; Growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; glycoprotein; phosphory
F;1-24/Domain: signal sequence #status predicted <NAT>
F;25-1210/Product: EGF receptor #status predicted <NAT>
F;25-645/Domain: EGF receptor extracellular domain repeat <EE1>
F;300/Domain: EGF receptor extracellular domain repeat <EE2>
F;46-668/Domain: intracellular #status predicted <TWM>
F;66-1210/Domain: protein kinase homology <KIN>
F;710-975/Domain: intracellular #status predicted <TWM>
F;718-725/Region: coated-pit mediated internalization signal
F;1047-1210/Region: inhibitory
F;138,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predic
                                             grow
                                         epidermal
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45.6%; Score 3116; DB 1; Length 1210;
Best Local Similarity 49.2%; Pred. No. 9e-121;
Matches 625; Conservative 179; Mismatches 355; Indels 112;
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A;Fille: Identification of residues in the nucleotide binding site
A;Reference number: A60143; MUID:85182650; PMID:2985580
A;Accession: A60143
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QY 244 CTGPKHSDCLACLHFNHSGICELHCPALVFNNFTVSFWLRVPKVSASHLERYTFGASCVT 303	OY 304 ACPYNYLSTDVGSCTLVCPLHNOEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVT 363	Qy 364 SANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPD 423 :	Qy 424 SLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFV 483 :	QY 484 HTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTOCVNCSOFLRG 543	QY 544 QECVEECRVLQGLPREYNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV 603	Qy 604 ARCPSGVKPDLSYMPIMKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA 663	OY 664 VVGILLVVVLGVVFGI-LIKRRQOKIRKYTWRRLLQETELVEBLFPSGAMPNQAQMRILK 722	Qy 723 ETELRKUKULGSGAFGTUYKGIMIPDGBNVKIPVAIKVLRENTSPKANKEILDBAYVMAG 782	Qy 783 UGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL 842 : :	QY 843 EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR 902	Qy 903 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV 962 :	QY 963 KCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMG 1021 DD	1022	Qy 1082 APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTC 1135	QY 1140 SPQPEYVNOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVEN 1195	QY 1200 PEXL-TPQGGAAPQPHPPAFSPAFDNLYYWDQDPPERGAPPST 1242	Qy 1243 FKGTPTAENPEYLGLDVP 1260 Db 1187 FKG-PTAENAEYLRVAPP 1203
R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B. Oncogene 6, 673-676, 1991 A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding sit A;Reference number: A43818; MUID:91232866; PMID:2030916 A;Accession: A43818	A; Molecule type: mRNA A; Residues: 1-714 < AVI> A; Cross-references: GB: X59698 D; Fishings D D: Correst D D	Submitted to the EMBL Data Library, June 1992 A;Reference number: S24942 A;Accession: S24942	A;MOJECULE TYPE: MKNA A;Residues; 969-971, KY, 973-1115, D' <eis> A;Cross-references: EMBL:Z12608 R;Heisermann, G'J.; Gill, G'N.</eis>	D. BLOLI CHEM. 209, 1332-1332-1330, 1350 A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylated i A;Reference number: A28941; MUID:88330814; PMID:3138233	A; Molecule type: procent A; Residues 689-684, X, 696-704, 'L', 706-707, 989-992, 'XX', 995-996, 'X', 998-1000, 1002-1009, R; Hibbs, M.L.; Dunn, A.R.; Alexander, W.S. Bubmitted to the EMBL Data Library, April 1994 A: Description: The complete cDNA esquence of the Mouse Bridermal Crouth Baston Document		A; Residues: 1-971, Kr, 973-1210 < VER.> A; Rcross-references: EMBL:X78987; NID:g488830; PIDN:CAA55587.1; PID:g488831 R; Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.	A;Title: Expression of the epidermal growth factor receptor gene is regulated in mouse E A;Reference number: 149643; MUID:93126380; PMID:7678348 A;Accession: 149643	A; Molecule type: mRNA A; Residues: 12-20,22-132 <res> A; Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201</res>	Cydenerics: Cydener EGFR C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Superfamily: epidermal growth factor receptor; kinase-related transforming protein; phosphopro F;1-74/Domain: signal sequence #status predicted <81G>	F;648-670/Domain: transmembrane #status predicted <tmm> F;712-977/Domain: protein kinase homology <kin> F;712-978/Region: protein kinase ATP-binding motif F;648-654/Region: protein kinase ATP-binding motif F;648-654/Rinding site: phosphate (Tht) (consider) #status opporting of the profile of the protein the protein of the protein the profile of the protein the protein the profile of the protein the profile of the profile o</kin></tmm>	F:697,1070,1071/Binding site: phosphate (Sev7) (covalent) #status experimental F:697,1070,1071/Binding site: (or 997) phosphate (Sev7) (covalent) #status experimental F:1028/Binding site: (or 1030 or 1032) phosphate (Sev7) (covalent) #status experimental F:11028/Binding site: (or 1030 or 1032) phosphate (Sev7) (covalent) #status experimental F:1107/Binding site: phosphate (Tyr) (covalent) #status experimental	Query Match 45.2%; Score 3092; DB 2; Length 1210; Best Local Similarity 49.1%; Pred. No. 8.7e-120; Matches 628; Conservative 171; Mismatches 363; Indels 116; Gaps 24;	Qy 11 LLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN 68	OY 69 ASLSFLQDIQEVQGYVLIAHNOVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128	Qy 129 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI 184	OY 185 DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAG 243 : :

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A47253
epidermal growth factor receptor, HER4 - human
epidermal growth factor receptor, HER4 - human
(S.Speciele: Homo appiens (man)
C.Dacession: A47253
R.Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.;
Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A;Tlitle: Ligand-specific activation of HER4/pl80erbB4, a fourth member of the epiderma
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AQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILD 775
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                                                                                                                                                                                                                                                                                                                                 FLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAHY
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A; Residues: 1-1223 <LLAX
A; Residues: 1-1223 <LLAX
A; Cross-references: GB:M2036
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.
Cell 41, 719-726, 1985
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro
A;Recession: A00643; MUID:8522822; PMID:2988784
A;Recession: A00643; MUID:8522822; PMID:2988784
A;Recession: A00643
A;Recession: B00643
A;Recession: A00643
A;Recession: B0064
C;Genetics:
A;Gene: erbB
C;Genetics:
A;Genetics:
A;Genetics
                                     Poidermal growth factor receptor precursor - chicken
N; Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C; Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C; Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C; Date: 28-Feb-1986
C; Date: 28-Feb-1986
C; Date: 28-Feb-1986
C; Date: 28-Feb-1986
C; Date: 28-Feb-2000
C; Date: 28-Feb-
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Matches 627; Conservative 176; Mismatches 349; Indels 151; Gaps
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                                                                                                                                                                                                                       Gaps
           A; Accession: A47253
A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-1308 < PLO>
A; Cross-references: GB: L07868; NID: g337359; PIDN: AABS9446.1; PID: g337360
A; Note: sequence extracted from NCBI backbone (NCBIP: 126842)
A; Note: sequence extracted from NCBI backbone; protein kinase homology
C; Superfamily: epidermal growth factor receptor; protein kinase homology
F;716-981/Domain: protein kinase homology «KIN»
F;724-732/Region: protein kinase ATP-binding motif
                                                                                                                                                                                      Query Match 43.4%; Score 2971.5; DB 2; Length 1308; Best Local Similarity 45.2%; Pred. No. 8.2e-115; Matches 612; Conservative 187; Mismatches 373; Indels 181;
A; Reference number: A47253; MUID: 93189574; PMID: 8383326
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protein-tyrosine kinase (BC 2.7.1.112) mrk-Y precursor - southern platyfish protein-tyrosine kinase (BC 2.7.1.112) mrk-Y precursor - southern platyfish (Species Xiphophorus maculatus (southern platyfish) (Species Xiphophorus maculatus (southern platyfish) (Species Xiphophorus maculatus (southern platyfish) (Species 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000 (Spacession: So6142; S1380) (Species Xi) Adam, D.; Adam, D.; Malitschek, B.; Maculer, W.; Raulf, F.; Telling, A.; Robe: Nature 341, 415-421, 1989 (MID: 90015140; PMID: 2797166 (MID: 415-421, 1989) (MID: 90015140; PMID: 2797166 (MID: 415-421, 1980) (MID: 90015140; PMID: 2797166 (MID: 415-421, 1980) (MID: 90015140; PMID: 2797166 (MID: 415-421, 1980) (MID: 90015140; PMID: 2797166 (MID: 90015140; PMID: 2797166 (MID: 415-421) (MID: 90015140; PMID: 1846957 (MID: 90015140; PMID: 1846957 (MID: 90015140; PMID: 1846957 (MID: 90015140; MID: 910125882; PMID: 1846957 (MID: 91025, MI); MID: 910265284; PIDN: CADA> (MID: 91025, MI); MID: 910265284; PIDN: CADA> (MID: 91025, MI); MID: 910265284; PIDN: CADA> (MID: 911025, MI); MID: 910265284; PIDN: CADA> (MID: 911025, MI); MID: 910265284; PIDN: CADA> (MID: 911025, MI); MID: 910265284; PIDN: CADA> (MID: 9110265285) (MID: 9100151); MID: 91001510; MID: 91
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A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C;Superfamily: epidermal growth factor receptor; phosphotransferase; transmembrane protein; C;Reywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; E;1-25/Domain: signal sequence #status predicted <SIG>E;26-1166/Product: Kinase-related transforming protein (Tu) #status predicted <MAT>E;707-972/Domain: protein kinase homology <KIN>E;715-723/Region: protein kinase ATP-binding motif
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                                         881
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942 PPICTIDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------PLAP-SEGAGSDVFDGDLGMG
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                                                                                                             890 VPIKWMALESILRRRFTHQSDVWSYGVTVWBLMTFGAKPYDGIPAREIPDLLEKGERLPQ
                                                                                                                                                                                                                                                      PPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNED-LGPASPLDS
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Length 1166;

Score 2674; DB 1; Pred. No. 1.2e-102;

39.1%;

Query Match Best Local Similarity

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нев 577; Conservative 160; Mismatches 384; Indels 160: Gaps 31:	4 AALCRWGLLLALLPPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 59	RCCSTDPD	60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119		GDPLANTTPVTGASPGGLRELQLRSLTEILKGGVLJQRNPQLCYQDTILWKDIFHKNNQL 17	ION-NESSEDVIQVGERQELGESNLIEILSGGVKVSHNPLLCNVETINWWDIVDKTSNP 17	180 ALTLIDTNRSRAHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE 238 18	QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVFNNFTVSFWLRVPKVSASHLE 29		294RYTEGASCVTACPYNYLSTDVGSCTLVCPLHNOEVTAEDGTQRCEKCSKPCARVCYG 350	286 PNIKYTFGAACVKECPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPRVCDG 343	51 LGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLE	1GIGSESNITAVNSINIKSFSNCIKINGDIILNKNSFEGDPHYKIGIMDPEHLWNLTTVK	411 EITGYLYISAWPDSLPDLSVFONLOVIRGRILHNGAYS-LTLOGLGISWLGLRSLRELGS 469	GLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGP	:: : :	28	516 GPTMCVSCLHVDRGGRCVASCNLLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGBGPAN 575	CVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCP	76 CSKSAHFQDGPQCIPRCPHGILGDGDTL-IWRYADRWGQCQPCHQNCTQGCSGPGLSGCR	650 AEQRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPS 709 5	710 GAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKA 769	~	770 NKEILDEAYVAAGVGSPYVSRLIGICLTSTVQLVTQLAPPGCLLDHVRENRGRLGSQDLL 829 : : :	NWCMQJAKGMSYLEDVRLVHRDLAARNYLVKSPNHVKITDFGLARLLDIDETEYHADGGK 88	NWCVQ1AKGMNYLEERHLVHRDLAARNVLLKNPNHVKITDFGLSKLLTADEKEYQADGGK 87	890 VPIKMMALESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIFAREIPDLLEKGERLPQ 949	950 PPICTIDVYMIMVKCMMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDIGPASPLDST 1009	1
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see-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human becies: Homo sapiens (man)
tte: 04-oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
cession: A36223; IS9164
aus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
tle: Isolation and characterization of ERBB3, a third member of the ERBB/epiderma.
ference number: A36223; MUID:90083234; PMID:2687875
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line GDB:ERBB3; HER3
ross-references: GDB:119880; OMIM:190151
ross-references: GDB:119880; OMIM:190151
ross-references: GDB:119880; OMIM:190151
ross-references: GDB:119880; OMIM:190151
line Description: 12413-12413
line Description: 12413-12413
line Description: Protein kinase homology «KIN»
lis-723/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                        ETDGYVAPLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLER 1175
                                                                                                                                                                                                                                                                                                                                                                                                                 1176 AKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPE 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GLLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT 67
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                                                                                                       ------ PVRENSITLRNISDPTONALEK
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oss-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1236 RGAPPSTFKGTPTAENPEYLG 1256
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                                                                                                       ------BPCIPPTGH-----
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Cyactes 17-041-1996 Hacqueince_revision 17-041-1998 Heat Condition 17-041-1998 Heat Cyactes 17-041-1996 Hacqueince_revision 19-041-1996 Hacqueince_revision 19-041-1996 Hacqueince_revision 19-041-1996 Hacqueince_revision 19-041-1999 Hacqueince_revision 19 36; 63 LEIVLTGHNADLSFLQWIREVTAYVLVAMNEFSVLPLPLPNLRVVRGTQVYDGKFAIFVM-- 120 120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179 121 ---ENYNT----NSSHALRQLKFTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRVR--- 170 60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119 238 283 GGVCVASCPHNFV-VDQTFCVRACPPDKMEVD-KHGLKMCEPCGGLCPKACEGTGSG--S 338 417 239 OCAAGCTGPKHSDCLACLHFNHSGICELHCP-ALVFNNFTVSFWLRVPKVSASHLERYTF 297 298 GASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLR 357 418 ISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHH 476 535 518 NCSOPLRGOECVEECRVLOGLPREYVNARHCLPCHPECOPONGSVTCFGPEADOCVACAH 595 578 3 LAALCRWGLLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 59 62 epidermal growth factor receptor homolog precursor - rat NyAlerande names: ExbB3 protein, HER3 protein C.Species: Rattus norvegicus (Norvay rat C.Species: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998 7 LOVLC----FILSLARGSEMGNSQAVCPGTLNGLSVTGDADNQYQTLYKLYEKCEVVMGN 180 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE 477 NTHLCFVHTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCV 459 NQQLCYHHSLNWTRLLRGPSEERLDIKYDRPLGECLAEGKVCDPLCSSGGCWGPAPGQCL 358 EVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLY Query Match 33.7%; Score 2306.5; DB 2; Length 1339; Best Local Similarity 40.3%; Pred. No. 1.6e-87; Matches 520; Conservative 173; Mismatches 434; Indels 163; Gaps ઠે 셤 셤 셤 g 셤 ò g ò g g ઠ ò δ ò ઠે δ g δ ď

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702 172 762 232 822

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1002 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG
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                                                                                                                                                                                                                          60 GP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP
                                                                                                                                                                                                                                                                                                      644 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEPLTPSGAMPNOAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
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                                                                                                                                 Gaps
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                                                                                                                                 125;
                                                                      Length 698
                                                                                                                             Indele
                                                                   DB 1;
                                                                                                                          80; Mismatches 137;
                                                                                                  1.1e-65;
                                                                25.8%; Score 1766.5; 52.2%; Pred. No. 1.1e
         ?;229/Active site: Lys #status predicted
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                                                                                               Similarity
                                                                Query Match
Best Local Simil
Matches 374; C
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C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999
C; Accession: B00643; A00643
R; Villsen, T. M.; Marconey, P. A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M. A; Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and prody A; Reference number: A00643; MUID:8522822; PMID:2988784
A; Reference number: A00643; MUID:8528222; PMID:2988784
A; Residues: 1-698 AVIL->
A; Residues: 1-698 AVIL->
A; Residues: 1-698 AVIL->
A; Residues: 1-698 AVIL->
A; Rose-references: GB:M10066; GB:M13881; NID:9211749; PIDN:AAA48763.1; PID:9211750
A; Note: in Genbank entry CHKRRBEF, release 109.0, the source is designated as Gallus gal C; Comment: This protein is synthesized as a gag-env-erbB protein.
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific processing the protein (fragment) #status predicted <GAG>
F; 1-6/Product: gag protein (fragment) #status predicted <GAG>
F; 1-6/Product: env protein (fragment) #status predicted <GAG>
F; 1-6/Product: env protein first winds the contable of the cont
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A;Reference number: S35743
A;Accession: S35745
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A;Residues: 1-544 <VEN>
A;Residues: 1-544 <VEN>
A;Cross-references: EMBL:X12707
A;Cross-references: EMBL:X12707
A;Cross-references: EMBL:X12707
A;Cross-references: EMBL:X12707
A;Conetion: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: norogene; phosphotransferase; transforming protein; tyrosine-specific
F;135-400/Domain: protein kinase homology <KIN>
F;143-151/Region: protein kinase ATP-binding motif
F;170/Active site: Lys #status predicted
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Best Local Similarity 54.9%; Pred. No. 7.1e-61;
Matches 345; Conservative 70; Mismatches 121;
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                                           A Residues: 1.28, W, 30-139, F, 141-145, V, 147-152 < DEB>
A; Cross-references: GB: K02006
C; Genetics:
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                                                                                                                                                                                                                                                                  Query Match 24.9%; Score 1703; DB 1; Length 604; Best Local Similarity 52.2%; Pred. No. 4e-63; Matches 360; Conservative 76; Mismatches 128; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-28,'W',30-139,'F',141-145,'V',147-152 <DEB>
Cross-references: GB:KO2006
Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1254
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R;Vennstroem, B.
submitted to the EMBL Data Library, March 1993
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         Accession: A38022
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A;Cross-references: GB:X52211
C;Genetics:
A;Gene: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein kinase
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;130-1395/Domain: protein kinase homology <KIN>
F;138-146/Region: protein kinase ATP-binding motif
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Best Local Simil
Matches 340; C
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A;Molecule type: DNA
A;Residues: 1-545 <SCO>
A;Cross.references: EMBL:X06943
C;Genetics:
A;Gene: erbB
C;Superfamily: epidermal growth factor receptor; pr.
C;Reywords: ATP; phosphotransferase
F;135-400/Domain: protein kinase homology <KIN>
F;143-151/Region: protein kinase ATP-binding motif
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Best Local Similarity 54.9%
Matches 345; Conservative
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                                                                     593 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                 59 NGSKTPSIAAGVVGGLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
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                                                                                                                                             RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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                                     Indels
23.7%; Score 1623; DB 2; I
llarity 54.9%; Pred. No. 6.8e-60;
Conservative 69; Mismatches 120;
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Job time : 31.0157 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 22, 2003, 08:12:49; Search time 10.2793 Seconds (without alignments) 5088.033 Million cell updates/sec Run on:

Perfect score: Title:

SEQ4-250-264-14 6839 1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1261 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description			σ,	m	P00533 homo sapien	Q01279 mus musculu			m		Q62799 rattus norv	P04412 drosophila			73 avian	37		_		P15208 mus musculu	P15127 rattus norv	P06213 homo sapien	Q9wtl4 mus musculu	P14616 homo sapien		_	_	P08069 homo sapien	O60751 mus musculu	~	'n	00		20
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ALIGNMENTS

| BREDLING. BREDLING. BREDLING. BREDLING. D. ERRIZ. HUMAN STANDARD; PRT; 1255 AA. P04657. P04657. P04657. P04657. P04657. P04657. P05. Late annotation update) DT 13-AUG-1987 (Rel. 05, Late annotation update) DT 13-AUG-1987 (Rel. 05, Late annotation update) BECEPLOT protein-Prosine kinase erbb-2 precursor (EC 2.7.1.112) BECEPLOT PROSINE PROM N.A. RAMMONING. SULT 1
B2_HUMAN
ERREZ HUMAN STANDARD; PRT; 1255 |
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CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR
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Matches 1240; Conservative
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                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; 1PR0001994; EGFR L domain.

Britisher; 1PR0001994; EGFR L domain.

Britisher; 1PR0001194; EUK_pkinase.

Britisher; 1PR0001145; Furin-like.

Britisher; 1PR001415; Tyr_pkinase.

Britisher; 1PR001415; Furin-like; 1.

Britisher; 1PR00145; Furin-like; 1.

Britisher; 1PR00145; Furin-like; 1.

Britisher; 1PR00145; Furin-like; 1PR00145; 1PR
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782, ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.206; SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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EMBL; M11761; AAA35808.1; JOINED.
EMBL; M11762; AAA35808.1; JOINED.
EMBL; M11764; AAA35808.1; JOINED.
EMBL; M11764; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M11766; AAA35808.1; JOINED.
EMBL; M11730; AAA35808.1; JOINED.
EMBL; M11730; AAA35808.1; -...
EMBL; X03363; CAA27693.1; -...
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Genew; HGNC:3430; ERBB2.
MIM; 164870; -.
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PIR; A24571; A24571.
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                                       AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMS
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MEDLINE=86118662; PubMed=3945311;
Bargmann C.I., Hung M.-C., Weinberg R.A.;
"The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 37, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p1885rbB2) (NEU prote-oncogene) (C-erbB-2) (Epidermal growth factor ERBB2 OR NEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
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MEDLINE=91222560; PubMed=2025425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
*** PERUCTURE BY NAMR OF 650-668.

*** MEDLINE-92155181; PubMed=1346763; MEDLINE-92155181; PubMed=1346763; MEDLINE-92155181; PubMed=1346763; MEDLINE-92155181; PubMed=1346763; MEDLINE-92155181; PubMed=1346763; MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLINE-MEDLI
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R HSSP, P11362, 17618.

R InterPro; IPR0001494; EdFR L domain.

InterPro; IPR0001494; Eurinitie.

R InterPro; IPR0012145; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Fam; PR00169; Pkinase; I.

R Fam; PR00130; Recep_L domain; 2.

R Fam; PR01030; Euk_pkinase; 1.

R ProDom; PD00001; Euk_pkinase; 1.

R MART; SM00261; FU; 2.

R SMART; SM00219; TyrKc; 1.

R PROSITE; PS00107; PR0TEIN KINASE_ATP; 1.

R PROSITE; PS00101; PR0TEIN KINASE_TYR; 1.

R PROSITE; PS0011; PR0TEIN KINASE_DW; 1.

R PROSITE; PS0011; PR0TEIN KINASE_TYR; 1.

R Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;

W Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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SPLAPSEGAGSDVFDGDLAMGVTKGLQSLSPHDLSPLQRYSEDPTLPLPPFTDGYVAPLA
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                                                                                                                                                            MSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALE
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                                                               VMAGVGS PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKG
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Mesocricetus auratus (Golden hamster).

Mesocricetus auratus (Golden hamster).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus

NCBI_TaxID=10036;
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SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNC-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (p185erbB2) (NEU proto-oncogene) (C-erbB-2).
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SUBUNIT: HETERODIME
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Best Local Similarity 86.5%;
Matches 1092; Conservative 5:
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R Pfam; PF00757; VLP; I.

R Probom; PF00150; Recep_L_domain; 2.

R Probom; PD000001; Euk_pkinase; 1.

R Probom; PD000001; Euk_pkinase; 1.

R PROSTTE; SM002019; TVTC; 1.

R PROSTTE; PS00109; PROTEIN KINASE ATP; 1.

R PROSTTE; PS00109; PROTEIN KINASE DOM; 1.

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Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; M Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Prote-oncogene; Disease mutation.

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InterPro; IPR000719; Euk Phinase.
InterPro; IPR00174; Furin-11ke.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004049; YLP motif.
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                                                                                                                                                          PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENP
                                                                                LAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCS
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=21100872; PubMed=11161793;
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MEDLINE=95382957; Pubmed=7654368;
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MEDLINE=97078686; PubMed=8918811;
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Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
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MEDLINE=85046483; PubMed=6093780;
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"Disulfide bond structure of human epidermal growth factor receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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"Analysis of the glycosylation patterns of the extracellular domain the epidermal growth factor receptor expressed in Chinese hamster
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TISSUE SPECITY: Expressed in placenta. Isoform 2 is also expressed in ovarian cancers.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kines activity, stimulation of cell synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
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MEDLINE=20198209; Pubmed=10731668;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. 127:65-72(2000)
and supercoiled DNA.";
Nature 309:270-273(1984).
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                                                                                                                           LLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
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                                                                                              112;
                                                                   Length 1210;
                                                                                              IndelB
                                                                                 al Similarity 49.2%; Pred. No. 4.5e-160; 625; Conservative 178; Mismatches 356;
                                                                   Score 3114; DB 1;
Pred. No. 4.5e-160;
                                                                   45.5%;
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1142 QPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPE 1201
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                                                                                                                                                                                                                                                                                                          1138 YLNTVQ------PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFK 1188
WMIDSECRPRFRELVSEFSRMARDPORFVVIO-NEDLGPASPLDSTFYRSLLEDDDMGDL 1023
                                                                                     1037 SLSATSN--NSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFL----P
                                                                   VDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAP
                                                                                                                                    1084 SEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSP
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STRANIBALBY.C, and CD-1; TISSUB=Liver, and Decidua;
STRANIBALBY.C, and CD-1; TISSUB=Liver, and Decidua;
MEDLINE=93126380; PubMed=7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The mouse waved-2 phenotype results from a point mutation in the EGF receptor tyrosine kinase.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=B6/C3; TISSUB=Liver;
STRAIN=B6/T10986; PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV1V1 A., Skorecki K., Yayon A., Givol D.; "Promoter region of the murine fibroblast growth factor receptor (bek/KGFR) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVCENTALION:
TISSUB-Brain;
MEDLINE=91232866; PubMed=2030916;
MEDLINE=91232866; PubMed=2030916;
Tax I., Ullrich A., Schlessinger J., Givol D., Morse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=93026370; PubMed=1408137;
Avivi A., Skorecki K., Yayon A., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Liver;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@aibe.sib.ch).
                                                         -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell DNA synthesis, and cell proliferation.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
EPIDERAL GROWTH FACTOR RECEPTOR.
EXTRACELLULAR (FOTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
APPROXIMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00101; PROTEIN KINASE TOW; 1.
Transmembrane; 01ycoprotein; Receptor; Signal; Transferase;
Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.
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ATP (BY SIMILARITY).
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InterPro; 1PR0000494; EGFR L domain.
InterPro; 1PR000119; Euk pkinase.
InterPro; 1PR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
Probom; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TYrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                   EMBL; X78987; CAA55587.1; -.
EMBL; U03425; AAA17899.1; -.
EMBL; X59698; CAA4222.9.1; -.
EMBL; L06664; AAA53029.1; -.
EMBL; Z12608; CAA78249.1; -.
                                                SEQUENCE OF 969-1117 FROM N.A.
           binding site.";
Oncogene 6:673-676(1991)
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LSSLSATSN----NSTVACINRNGSCRVKEDAFLQRYSSDPTGAVTEDNIDDAFL----
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                                           ARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA
                                                              VVGILLVVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK
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BDDLINE=29189574; PubMed=8181126;
Plowman G.D., Culouscou J.-M., Whitney G.S., Green J.M., Carlton G
Foy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HER4/p180erbB4, a fourth member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DC-1998 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
(p180erbB4) (Tyrosine kinase-type cell surface receptor HER4).
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FKG-PTAENAEYLRVAPP 1203
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-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORNS; JM-A (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORNS DIFFER FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORNS ARE EXPRESSED IN CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.
-1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART, KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CEREBELLUM, PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS, LUNG, SALIVARY GLAND, AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000494; EGFR L domain.

InterPro; IPR000199; Euk pkinase.

InterPro; IPR000214; Furin-like.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001249; YLP_motif.

InterPro; IPR001249; Y
                                                                                                                                                  "A novel juxt, amembrane domain isoform of HER4/ErbB4. Isoform-specific tissue distribution and differential processing in response to phorbol ester.";

J. Biol. Chem. 272:26761-26768 (1997).

-!- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, HEPARIN BINDING EGF-LIKE GROWTH FACTOR, BETACELLUIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.

NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.

-!- CARTAVTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
                                                                           TISSUE=Fetal brain;
MEDILNES97476287; PubMed=9334263;
Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
Klagsbrun M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
CYS-RICH.
CYS-RICH.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993)
                                                           SEQUENCE FROM N.A. (ISOFORMS JM-A AND JM-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L07868; AAB59446.1; -. HSSP; P11362; 1FGK.
Genew; HGNC:3432; ERBB4.
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SIGNAL 1 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 KKCPHNFV-VDSSSCVRACPSSKMEV-EENGIRMCKPCTDICPKACDGIGTGSLMSAQTV
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ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

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BY
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648
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(EC 2.7.1.112)

Receptor protein-tyrosine kinase erbB-4 precursor ERBB4 OR TYRO-2.

Rattus norvegicus (Rat)

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PPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNED-LGPASPLDS 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1100 AAKGLQSLPTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVR 1152
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                                                                              469 YHINWTTLFSTINQRIVIRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFSR
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                                                                                                                                                                                                                                                        1050 HSPPPAYTPMSGNQFVYRDGGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF
                                                               VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR
                                                                                                           GQECVEECRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFGPEADQCVACAHYKDPPF
                                                                                                                                                       CVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC-----PA
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062956; 0922N7; 15-DEC-1998 (Rel. 37, Created) 15-JUN-2002 (Rel. 41, Last sequence update)

STANDARD;

ERB4 RAT

RESULT 7

ERB4_RAT ID ERB4 AC Q629 DT 15-D DT 15-J

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                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREFERENTALLY EXPRESSED IN THE DEVELOPING
NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                                                                                                                                                                                                                                                                                                                    Lai C., Lemke G.; "An extended family of protein-tyrosine kinase genes differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
RECEPTORS (POTENTIAL).
                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                            "Neuregulins promote survival and growth of cardiac myocytes. Persistence of ErbB2 and ErbB4 expression in neonatal and adult ventricular myocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY). SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                 MEDLINE=98221155; PubMed=9553078;
Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han X.,
Marchionni M.A., Kelly R.A.;
                                                                                                                                                                                                                                                                                                                                                      expressed in the vertebrate nervous system.";
                                                                                                                                                                                                                                             Biol. Chem. 273:10261-10269(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000494, EGFR L domain.
Interpro; IPR000719; Euk pkinase.
Interpro; IPR002174; Purin-like.
Interpro; IPR004019; Yr pkinase.
Interpro; IPR004019; Yr motif.
                                                                                                                                                                                                                                                                                        TISSUE=Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
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Pfam; PF02757; YLP; Z.
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                                                         Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00757; Furin-like; 1. Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                          SEQUENCE OF 848-901 FROM N.A.
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                                                                                                                      SEQUENCE FROM N.A.
                                                                                          NCBI_TaxID=10116;
                                                                                                                                      TISSUE=Heart
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475 461 648 639 762

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KGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNED-LG 1001
                                                                                                                                                                                                                                                                                                                                                                                   VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
                                                               TFGASCVTACPYNYLSTDVGSCTLVCPLHNOEVTAEDGTORCEKCSKPCARVCYGLGMEH
                                                                                                                                                                                                                       LMSAQTVDSSNIDKFINCTKINGNLIFLYTGIHGDPYNAIDAIDPEKLNVFRTVREITGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHSTLPQHAR-TPL--IAAGVIGGLFILVIMALTFAVYVRRKSIK-KKRALRRFL-ETEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETTGPKANVEFMDBALIMASVDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLEYVHEHKDN
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                                           178 QLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCC
                                                                                                                    HEQCAAGCTGPKHSDCLACLHFNHSGICELHCP-ALVFNNFTVSFWLRVPKVSASHLERY
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SMART; SM00261; FU; 4.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE TOM; 1.

Transmembrane; Glycoprotein; Miltigene family; Receptor; Signal; Transferase; Tyrosine-protein Kinase; ATP-binding; Phosphorylation. SIGNAL 25 TOTOLEIN KINASE; ATP-binding; Phosphorylation. 25 TOTOLEIN KINASE; ATP-binding; Phosphorylation.
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         ---PPKAEDEYVNEPLYLNTFTNALGNAEYMKNSLLSVPEKAKKAFDNPDYWNHSLPPRS 1251
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SMART; SM00220; ZTKC; 1.
SMART; SM00219; TYrKC; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00100; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
Tyrosine-protein kinase; ATP-binding; Phosphorylation; Proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112)
XMRK OR TU.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Crāniata; Vertebrata, Euteleostomi, etafinopterygii, Neoperygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha; Cyprinodontiformes, Poeciliidae, Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=90015140; PubMed=2797166;
Wittbrodt J., Adam D., Malitschek B., Maueler W., Raulf F.,
Telling A., Robertson S.M., Schartl M.;
"Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu locus in Xiphophorus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MELANOMA RECEPTOR PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNAT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                              A--PPSTFKGTPT-----AENPEYL 1255
                                                                                           1252 TLQHPDYLQEYSTKYFYKQNGRIRPIVAENPEYL 1285
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PIR; S06142; S06142.
HSSP, P11362; 1FGK.
INTERPO, IPR000494; EGFR L domain.
INTERPO; IPR000719; Furin-like.
INTERPO; IPR002174; Furin-like.
INTERPO; IPR002290; Ser thr pkinase.
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ProDom; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 5.
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(Rel. 40, Last seq
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Pfam, PF00757, Furin-like, 1.
Pfam, PF01030, Recep_L_domain
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                                                          GNVILKNTLOLRYANTINWRRLFRSEDOSIEYDART-----ENOTCNNECSEDGCWGP
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Eukaryota; Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(C-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
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15-JUN-2002 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECRETED (SHORT FORM).

-!-ALTERNATIVE PRODICTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
-!- DOMAIN: THE CYTOPLASHIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-!- PTM: LIGAND-BINDING INTERACES PHOSPHORYLATION ON TYROSINE RESIDUES PHOSPHORYLATION AND TROOPES ITS ASSOCIATION WITH THE PRES SUBUNIT OF PHOSPHORYLINGS.
-!- DISEASE: OVEREXRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.
-!- BISEASE: OVEREXRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.
                                                                                                                                                                                                 MEDLINE=90311312; PubMed=2164210; Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L., Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L., Todaro G.J., Shoyab M.; Molecular cloning and expression of an additional epidermal growth factor receptor-related gene."; Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990).
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Pram; PP00069; prinase; 1.
Pram; PP001030; Recep_L domain; 2.
ProDom; PD000001; Buk_prinase; 1.
SWART; SM00261; FU; 3.
SWART; SM00219; TyrKc; 1.
PROSITE; PS001019; PROTEIN KINASE ATP; PALSE NEG.
PROSITE; PS001019; PROTEIN KINASE TYR; FALSE_NEG.
PROSITE; PS001019; PROTEIN KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Transmembrane; Glycoprotein kinase; ATP-binding; Phosphorylation;
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                                                 MEDLINE=90083234; PubMed=2687875;
Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.;
"Isolation and characterization of ERBB3, a third member of the ERBB/epidermal growth factor receptor family: evidence for overexpression in a subset of human mammary tumore.";
Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197 (1989).
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                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93282822; PubMed=7685162;
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InterPro, IPR002174; Furīn-like.
InterPro, IPR001245; Tyr pkinase.
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 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SHI DOMAIN: OF MANY SIGNAL-TRANSDUCING PROTEINS.
-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00261; FU; 5.
SMART; SM00219; TYYKC; 1.
PROSITE; PS00100; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00100; PROTEIN KINASE TYR; 1.
TRANSMEMBRANE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                SEQUENCE OF 922-1097 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE-Sciatic nerve;
MEDLINE-97184212; PubMed=9030624;
MEDLINE-97184121; PubMed=9030624;

"Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997)
J. Neurosci. 17:1642-1659(1997)
J. FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-! CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                       STRAIN=Sprague-Dawley; TISSUE=Liver; MEDLINE=96096535; PubMed=8522190; Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.; "Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.";
 15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(c-erbB3)
                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                     [2]
REVISIONS TO 85, 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U29339; AAC28498.2; ---
EMBL; U52530; AAC53050.1; ---
HSSP; P1136.2; 1FGK.
INTEPPO; IPR000949; EGFR L domain.
INTEPPO; IPR000199; EUK PKInase.
INTEPPO; IPR00119; EUK PKInase.
INTEPPO; IPR001145; TYL PKINASE.
PKam; PP00069; PKINASE; 1.
PKam; PP00130; PKINASE; 1.
PKam; PF00130; RCCCP L domain; 2.
PRINTS; PR00109; TYRKINASE.
PKINDS; PR00109; TYRKINASE.
                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                       Gene 165:279-284 (1995)
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
15-DEC-1998
15-JUN-2002
15-JUN-2002
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OAASF2402BBFDF1E CRC64;
CYTOPLASMIC (POTENTIAL)
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ATP (BY SIMILARITY).

BY SIMILARITY.

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                                          NTHLCFVHTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCV
                                                                                                 NCSQFLRGOECVEECRVLOGLPREYVNARHCLPCHPECQPONGSVTCFGPEADQCVACAH
                                                                                                                                                        YKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSC---VDLDDKGCPAEQR
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REQUENCE FROM N.A. (ISOPORM TYPE I).

REQUIRED STRAIN-BERKELEY.

RA Addams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

Addams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.

RA Addams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Adril M.R., Doyle C., Baxrer E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RA Adril J.F., Agbayani A., An H.-J., Andrews Pfennkoch C., Baldwin D.,

RA Adril G.K., Busam D.A., Berman B.P., Bhandari D., Bolshakov S.,

Berson K.Y., Benos P.V., Berman B.P., Brottier P.,

RA Burtis K.C., Busam D.A., Bulke C., Dayenport L.B., Davies P.,

RA Glerry J.M., Cawley S., Dahlke C., Dayenport L.B., Davies P.,

RA Geblos B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,

RA Doubin K.J., Evangelista C.C., Ferrara C., Ferriera S., Pleischmann W.,

RA Dubin K.J., Evangelista C.C., Ferrara S., Pleischmann W.,

RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.B., Hauck J.,

RA Hostin D., Houston K.A., Hovland T.J., Wein M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Merkulov G., Milshina N.V., Mobarts S., Morris J., Morris J., Morris J.,

RA Harris N.W., May M., Murphy B., Murphy L., Muzny D.M., Nelson D.,

RA Reinert K., Remington K., Samders R., Vencese M.G.,

RA Reinert K., Remington K., Samders R., Vencese M.G.,

RA Shie B.C., Sident-Klamos I., Simpson M., Strong R., Smith T.,

Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,

Rang Z.-Y., Wassarman D.A., Weinstor C.M., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANALYSIS.
MEDLINE-99102120; PubMed=9882502;
MEDLINE-99102120; YU S.-Y., Katz J., Baker N.E.;
"Several levels of EGF receptor signaling during photoreceptor specification in wild-type, Ellipse, and null mutant Drosophila.";
Dev. Biol. 205:129-144(1999).
                                                                                                                                                 receptor homolog reveals
                                                                                                                                                              that several genetically defined classes of alleles cluster in subdomains of the receptor protein.";

Genetics 137:531-550(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=85124611; PubMed=2982499;
Livneh E., Glazer L., Segal D., Schlessinger J., Shilo B.-Z.;
"The Drosophila EGF receptor gene homolog: conservation of bot
hormone binding and kinase domains.";
                                                                                                                                                                                                                                                                                                           Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                      AND ALTERNATIVE SPLICING
                                                                           TYPES I AND II)
                                                                                                                  Clifford R., Schupbach T.; "Molecular analysis of the Drosophila EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM TYPE I).
                                                                      SEQUENCE FROM N.A. (ISOFORMS TYPES
MEDLINE=94350209; PubMed=8070664;
                                                                                                                                                                                                                                                                                     R., Schupbach T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 46:1091-1101(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF receptor.";

Cell 89:13-16(1997).

-! FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.
CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE COCYTE IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMNIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATE SETTICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE, UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92038942; PubMed=1936959;
Raz E., Schejter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for
the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perrimon N., Perkins L.A.; "There must be 50\ \text{ways} to rule the signal: the case of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
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                                                                                                                                                                          STRAIN=Daekwanryeong;
MEDLINE=85137938; PubMed=2983232;
Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
"A Drosophila genomic sequence with homology to human epidermal growth factor receptor.";
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EMBL; AF052753; AAC08536.1; --
EMBL; AF052754; AAC08535.1; --
EMBL; AF052754; AAC08535.1; --
EMBL; K03054; AAA51467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97248481; Pubmed=9094709;
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                                                                                                                                                     SEQUENCE OF 959-1078 FROM N.A.
                                                                                                           Science 287:2185-2195(2000).
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Best Local Similarity 32.5%; Pred. No. 6.2e-96;
Matches 465; Conservative 185; Mismatches 436; Indels 344; Gaps
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BUDERNAL GROWTH FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).

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                                                      714 GY--FWEYVHPQEQGSLKPLAGRAVCRKCHPLCELCTNYGYHEQVCSKCTHYKRREQCET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP--- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 RASPLTSIVSAVV-GILLUVVULGUVFGILIKRRQQKIRKYTMRRLLQGTELVEPLTPSGA
                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANGOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS NO SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY THE INSERTION OF RETROVIERE LEMENTS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

MISCELLANGOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=8522822; PubMed=2988784;
Nilsen T.W., Marconey P.A., Goodwin R.G., Rottman F.M.,

Crittenden L.B., Raines M.A., Kung H.-J.;

"c-exbB activation in ALV-induced erythroblastosis: novel RNA

"c-exbB activation in ALV-induced erythroblastosis of an

"c-exbB activation in ALV-induced erythroblastosis. Cover RNA

"c-exbB activation in ALV-induced erythroblastosis of an

"c-exbB activation in ALV-induced erythroblastosis of an

amino-truncated EGF receptor.";

Cell 41:719-726(1985).

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                     21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6%; Score 1749.5; DB 1; Length 52.3%; Pred. No. 4.5e-87; .ive 79; Mismatches 135; Indels
                                                                                                                                                                   Viruses, Retroid viruses, Retroviridae, Alpharetrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 ATP (BY SIMILARITY).
165 ATP (BY SIMILARITY).
257 BY SIMILARITY.
70891 MW: E705E33A0BE01FCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                     634 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE
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PRINTS; PR00109; TYRKINASE.

ProDom; P0000001; Euk_pkinase; 1.

SMART; SM00219; TYRKC; 1.

PROSITE; PS001107; PROTEIN KINASE ATP; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; MIUUGO; TOTALIN, A00643; TVCHLV. PIR; B00643; TVCHLV. HSSP; P11362; IFGK. InterPro; IPR00719; Buk pkinase. InterPro; IPR001245; TYT pkinase.
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M10066; AAA48763.1; ALT_INIT
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                   STANDARD:
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165
                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
                                                                                                                                                    Avian leukosis virus.
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634 AA;
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Best Local Simi
Matches 370;
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                   ERBB ALV
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BINDING
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712 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANK 771

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Phosphorylation.
                                                                                                                                                                                                                                                                                   67633 MW;
                                                                                                                                                                                                                                                                                                   Query Match 24.9
Best Local Similarity 52.2
Matches 360, Conservative
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257
29
140
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146
146
1604 AA;
                                                                                                                                                                                                                Glycoprotein;
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CONFLICT
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                                                                                                                            ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF 1010
                                                                                                                                                             1011 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1070
                                                                                                                                                                                               1071 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1125
                                                                                                                                                                                                                               1126 LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1183
                                                                                                                                                                                                                                                                 -----AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY 1228
                                                                                                                                              417
                         831
                                          237
                                                          891
                                                                           297
                                                                                                    298 IKWMALESILHRIYTHQSDVMSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPP 357
892 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.

DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS IN CHICKENS.
                                                         O.T. TAMVQ
                         EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84026539; PubMed-6313229;
Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima
"The erbB gene of avian erythroblastosis virus is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                retroviruses
                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                  WDQ------DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1260
                                                                                                                                                                                                                                                                                                                   625
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                                                                                                                                                                                                                                                                                                                                                                                                                 Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C
NCB1_TaxID=79685;
                                                                                                                                                                                                                                          496 FLEESIDDGFL-----PAPEYVNQ--LMPKKPS-
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                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene family.";
Cell 35:71-78(1983).
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P00535;
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MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE RECEPTOR FOR EPIDERMAL GROWTH FACTOR. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CAHFIDGPHCVKACPAGVLGENDTL-VRKYADANAVCQLCHPNCTRGCKGPGLEGCP-
                                                                                                                                                                                                                                                                                                              EMBL; K02006; AAA42394.1; ALT_INIT.

R PER, A00644; TVUVUH.

R HSSP, P11362; 1FGK.

R InterPro; 1PR000719; Euk pkinase.

R InterPro; 1PR00069; pkinase.

R InterPro; 1PR00069; pkinase.

R Probom; P000060; pkinase; 1.

R Probom; P00010; pkinase; 1.

R PROSITE; P800107; PROTEIN KINASE ATP; 1.

R PROSITE; P800109; PROTEIN KINASE DATP; 1.

R PROSITE; P850011; PROTEIN KINASE DOM; 1.

M Transferase; TYCOSING—TOM; PROTEIN KINASE—DOM; 1.

M Glyconrotein: Dhosobor-initials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.9%; Score 1703; DB 1; Length 604; 52.2%; Pred. No. 1.4e-84; ive 76; Mismatches 128; Indels 120
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
R -> W (IN REF. 2).
S -> F (IN REF. 2).
I -> V (IN REF. 2).
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NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE 117
                                                   553 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
  CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
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EGFR CHICK
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                                                                                                                                                      1184 NGVVKDVFAF-----GGAVENPEYLTPQGGAAPQPHPPPAFSPAFD 1224
                                                   1126 LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1183
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----SRTPLLSSLSATSNNSATNCID-----RNGQGHPVREDSFVQRYSSDPTGN 495
                                                                                                                                                                                                         --VONOIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNOSPLAKTVFE 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87064458; PubMed=2878364; Choi O.C., Trainor C., Graf T., Beug H., Engel J.D.; Arainor C., Graf T., Beug H., Engel J.D.; As ingle amino acid substitution in v-erbB confers a thermolabile phenotype to ts167 avian erythroblastosis virus-transformed erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avian erythroblastosis virus (strain ts167).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=103898;
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CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
H -> D (IN THERMOLABILE V-ERBB).
W; 5B53297AA068B65D CRC64;
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PROSITE; PSO109; PROTEIN KINASE TYR; 1.
PROSITE; PSO111; PROTEIN KINASE DOM; 1.
TABREFEASE; TYZESINE-PROTEIN KINASE DOM; 1.
Glycoprotein; Phosphorylation.
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55.1%; Pred. No. 1e-80;
iive 69; Mismatches 119; Indels
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                                                                                   01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein (V-ERBB.
                                                                                                                                                                                                                                                       NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1254
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InterPro; IPR000719; Buk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
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771
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Lax I., Johnson A., Howk R., Sap J., Bellot F., Winkler M.,

Ullrich A., Vernstrom B., Schleesinger J., Givol D.;

Chicken epidermal growth factor (EGF) receptor: cDNA cloning,

expression in mouse cells, and differential binding of EGF and

transforming growth factor alpha.";

Mol. Cell. Biol. 8:1970-1978(1988).

-I. FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,

AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND

VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                              358 ICTIDVYMIMVKCMMSDADSRPKFRELIAEFSKMARDPPRYLVIQGDERMHLPSPTDSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                           1011 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
712 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                    EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                                                                                                                                                          CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (CER)
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
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-----SHSTAVDNPEYL 539
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CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ

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MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell DNA synthesis, and cell proliferation.
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InterPro; IPR000494; EGFR L domain.

InterPro; IPR0002174; Furin-like.

InterPro; IPR0012174; Furin-like.

InterPro; IPR001245; TYr phinase.

Pfam; PF01030; Fecep L domain; 2.

RMART; SM00051; FU; Furin-like; 1.

RMSSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.

RROSITE; PS00109; PROTEIN KINASE DOM; PARTIAL.

RROSITE; PS0011; PROTEIN KINASE DOM; PARTIAL.

RROSITE; PS0011; PROTEIN KINASE DOM; PARTIAL.

RROSITE; PS0011; PROTEIN KINASE DOM; PARTIAL.

RYCOSINE-PROTEIN KINASE DOM; PARTIAL.

R TANNSMEM FACTOR RECEPTOR:

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EPIDERMAL GROWTH FACTOR RECEPTOR.

T FRANSMEM 655

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POWNIN 31 654

EVENTRALELLULAR (POTENTIAL).

POWNIN 500
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CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

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                      LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD
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                                                                                                                                    CAAGCTGPKHSDCLACLHFNHSGICELHCPALVFNNFTVSFWLRVPKVSASHLERYTFGA
                                                                                                                                                                                                                      SCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREV
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RGAAVLVLLLLGVALCSAVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLE
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                                                                       PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL
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completed: July 22, 2003, 08:45:38 Search

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 22, 2003, 08:22:34; Search time 48.5887 Seconds (without alignments) 5347.444 Million cell updates/sec Run on:

SEQ4-250-264-14 6839 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261 Perfect score:

Sequence:

671580 segs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

671580

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 21:* Database :

sp_plant:*
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sp_vertebrate:*
sp_unclassified:* sp_archea:*
sp_bacteria:*
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sp_tung1:*
sp_invertebrate:*
sp_mammal:*
sp_organe1le:*
sp_organe1le:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q99X70 rattus norv Q99S9 mus musculu Q9y40 xiphophorus Q9w6f6 gallus gall P79754 fugu rubrip Q9bh19 anopheles g Q9bk79 homo sapien Q812x1 mus musculu Q8714 avian rous-Q86714 avian rous-Q86714 avian rous-Q86495 avian eryth Q95468 avian eryth Q9w75 mus musculu Q9erv6 mus musculu 018735 canis famil Description 018735 Q9QX70 Q9EP98 Q9W6F6 P79754 Q9BH9 Q9BK211 Q8E712 Q86714 Q64895 Q85468 Q9WVF5 Q9ERV6 13 Query Match Length DB Score 6191 3119 3090 2020 2704.5 2011.5 1770.5 1770.5 1739 1739 1739 1739 1740.5 1693.5 1645.5

O9v1x8 ephydatia f			Q90836 gallus gall	Q9ese0 rattus norv	Q9psh2 gallus gall	Q14256 homo sapien	Q923v5 rattus norv	P11776 xiphophorus	Q8szwl drosophila	Q99162 xiphophorus	Q9pvz4 xenopus lae	Q9njv5 biomphalari	Q8uw85 paralichthy	093457 scophthalmu	Q9bud7 homo gapien	O8uw86 paralichthy	O73798 xenopus lae	Q9u5a8 bombyx mori	Q8uw84 paralichthy	Q9ygh8 scophthalmu	Q8uw83 paralichthy	Q9qvw4 rattus sp.	Q9bg66 oryctolagus	Q9vd94 drosophila	Q91ym0 mus musculu	Q07912 homo sapien	OS4967 mus musculu	Q9umg4 homo sapien
09Y1X8	023821	026566	090836	Q9ESE0	Q9PSH2	014256	Q923V5	P11776	Q8SZW1	099162	Q9PVZ4	Q9NJV5	QBUWB5	093457	Q9BUD7	QBUW86	073798	Q9U5A8	Q8UW84	Q9YGH8	QBUWB3	090VW4	09BG66	Q9VD94	Q91YM0	007912	054967	Q9UMQ4
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18.1	16.9	16.8	16.1	14.3	14.2	13.2	13.0	11.8	11.4	11.0	10.9	10.6	10.4	10.3	10.1	10.0	6.6	9.6	9.5	9.5	9.4	9.3	9.1	6.8	9.8	9.8	9.8	9.6
1240	1157.5	1146	1103	976.5	969.5	906	887	806.5	778	754.5	745.5	725	713.5	702	694	686.5	678	656.5	651	647	644.5	635	619	610.5	589	587.5	587.5	586.5
17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

	PRELIMINARY; PRT; 1259 AA.		(TrEMBLrel.	(TrEMBLrel.	(TrEMBLrel. 21, Last		Canis familiaris (Dog).	Metazoa; Chordata; C	Eutheria; Carnivora; Fissipedia; Canidae;)=9615;		CE FROM N.A.		"cDNA cloning of erbB-2 from canine mammary gland.";	197) to the			IPR002048;		IPR000719;	IPR002174;	IPR001245; Tyr	IPR004019;	Furin-lik		PF01030; Recep_L_domain; 2.	PF02757; YLP; 2.	ProDom; PD000001; Euk pkinase; 1.	SM00261; FU; 3.	SM00219; TyrKc; 1.	; PS00018;	PS00107;	PS50011;	109; PROTEIN	Transferase; Tyrosine-protein kinase.	JE 1259 AA; 137989 MW; E37364D49C4ACD46 CRC64;
35	018735	018735;	01-JAN-1998	01-JAN-1998	01-JUN-2002	ErbB-2.	Canis fam	Eukaryota	Mammalia;	NCBI TaxII	[1]	SEQUENCE FROM	Yokota H.;	"CDNA clo	Submitted	EMBL; ABO	HSSP; P11	InterPro;	InterPro;	InterPro;	InterPro;	InterPro;					Pfam; PF0	ProDom; PI	SMART; SM	SMART; SM	::			PROSITE; 1	ATP-binding;	SECUENCE
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1193 1255

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"A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively spliced transcript in normal rat tissue.";
                                                                                              LAPSEGAGSDVFDGDLGMGAAKGLQSLPSQDPSPLQRYSEDPTVPLPPETDGKVAPLTCS
                                                                                  PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLER-----AKTLSPGKNGVVKDVFAFGG
                                      LAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCS
                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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SMART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Receptor; Transferase; Tyrosine-protein kinase.
SEQUENCE 1209 AA; 134891 MW; 96FEE7F6CC1B7773 CRC64;
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MEDLINE=90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J.,
                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
Guttridge K., Dawson T.L., Earp H.S.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ dat
EMBL; M37994; AAF14008.1;
HSSP; P11362; PFCK.
InterPro; IPR00019; Euk pkinase.
R InterPro; IPR00019; Euk pkinase.
R InterPro; IPR001245; Tyr pkinase.
R Pfam; PF00069; pkinase; 1.
R Pfam; PF01009; Recep L domain; 2.
R PRINTS; PR00109; TYRKINASE.
R PRINTS; PR00109; TYRKINASE.
R PRODOUGH; Euk pkinase; 1.
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Pred. No. 7.8e-227;
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Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STAN-PISHER; TISSUE=LIVER;
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STRAIN=FISHER; TISSUE=LIVER;
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Best Local Similarity
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                                              MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                          Gaps
                         12;
   Length 1259;
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  DB
 90.5%; Score 6191; D 90.6%; Pred. No. 0; ive 41; Mismatches
Query Match 90.5
Best Local Similarity 90.6
Matches 1147; Conservative
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Lee D.C.,

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LCYANTINWKKLFGTPNQKTKIMNRAEKDCKATNHVCNPLCSSEGCWGPEPTDCVSCQN
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   Gaps
   Mismatches 358; Indels 120;
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                                                             1031 SRTPLLSSLSANSN----SSTVACINRNGSCRVKEDAFLQRYSSDPTSVLTEDNIDDTFL
                                                                                                                          1135 APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG
                                                                                                                                                                          GAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERG
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STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
Stater J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
Maihle N.J.;
"Comparative genomic sequence analysis and isolation of human and
mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CS7BL/6J,
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balagubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence analysis and isolation of human and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor isoform 1.
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EMBL, AF275366, AAG28045.1; -
EMBL, AF275366, AAG28045.1; -
EMBL, AF275367, AAG28045.1; -
HSSP, P11362, 1RGK.
HSSP, P11362, 1RGK.
MGD, MGI:95294, EGfr.
InterPro; IPR0000345; CytC. heme bind.
InterPro; IPR000145; EWE pkinase.
InterPro; IPR000197; EWE pkinase.
InterPro; IPR000197; EWE pkinase.
InterPro; IPR001274; FWIIn-like.
InterPro; IPR001296; Ser thr pkinase.
InterPro; IPR001296; Tyr pkinase.
Pfam; PF00109; Pkinase; 1.
Pfam; PF00109; TYRKINASE.
ProDom; PD000001; EWE pkinase; 1.
PRNNTS; PR00109; TYRKINASE.
PRODOSE; FU; 5.
SWART; SN00220; S.TKC; 1.
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PEYLNTAQ------PTCLSSGFNSPALMIQKGSHQMSLDNPDYQQDFFPKETKPNGI 1186
                                                                                                                                                   891 RIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIMV
                                            KCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMG
                                                                                                                                                                                                                                                                                              1140 SPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVEN
                                                                                                                                                                                                                                                                                                                                                                               ------DP-----PERGAPPST
                                                                                                                                DLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPL
                                                                                                                                                                                                               1082 APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTC
                                                                                                                                                                                                                                                     1037 LSSLSATSN----NSTVACINRNGSCRVKEDAFLQRYSSDPTGAVTEDNIDDAFL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xiphophorus xiphidium.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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STRAIN=RIO PURIFICATION;
MEDLINE=98241172; PubMed=9582016;
Dimitrijevic v. winkler C., Wellbrock C., Gomez A., Di
Altschmied J., Schartl M.;
"Activation of the Xmrk proto-oncogene of Xiphophorus overexpression and mutational alterations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NAY-1999 (TrEMBLrel. 10, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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HSSP; P11362; 1FGK.
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||| :|:|||||||||||||||
ETEFKKIKVLGSGAFGTVYKGLMIPEGEKVKIPVAIKELREATSPKANKEILDEAYWAS 770
                                                                                                                                                                                                                                                                                                          ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                                                                                                                                                                                                                                                                                                                                                                            129 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGPKHSDCLACLHFNHSGICELHCPALVFNNFTVSFWLRVPKVSASHLERYTFGASCVT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 ACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVT 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 ARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
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                                                                                                                                                                                         Gaps
                                                                                                                                                                                       Indels 116;
                                                                                                                                               DB 11; Length 1210;
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Receptor; Transferase.
SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
                                                                                                                                            tch 45.2%; Score 3090; DB 11; al Similarity 49.1%; Pred. No. 1.2e-224; 628; Conservative 170; Mismatches 364;
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1172 TLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQ 1231
                                                                                                                                     1006 LDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDL
                                                                                                                                                                                                                                                                                                             RLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASP
                                                  -------PVRENSIALRYISDPTON
                                                                                                                                                                                                                                                                                     1125 PLPSETDGYVAPLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGA
                                                                                                                                                                                                1066 TLGLEPSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 1137;
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BDLINE=929263203; PubMed=10328884;
Dixon M., Lumsden A.;
Distribution of neuregulin-1 (nrgl) and erbB4 transcripts embryonic chick hindbrain.";
Mol. Cell. Neurosci. 13:237-258(1999).
EMBL; AF121963; AAD31764.1; --
HSSP; P11362; 1FGK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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INTERPOS, PROMOTOS, ENK DKINAGE.
INTERPOS, IPROMOTOS, ENK DKINAGE.
INTERPOS, IPROMOTOS, ENK DKINAGE.
INTERPOS, IPROMOTOS, TYT DKINAGE.
INTERPOS, IPROMOTOS, TYT DKINAGE.
INTERPOS, IPROMOTOS, YLP MCTÍF.
PÉAM; PFONOTOS; PENTIN-LIKE; I.
PÉAM; PFONOTOS; PENTIN-LIKE; I.
PÉAM; PFONOTOS; PENTIN-LIKE; I.
PRAMITS; PROMOTOS; TYRKINAGE.
PRODOM; PROMOTOS; TYRKINAGE.
PROSTIE; PROMOTOS; TYRK, I.
PROSTIE; PSOMOTOS; TYRK, I.
PROSTIE; PSOMOTOS; PROTEIN KINAGE ATP; I.
PROSTIE; PSOMOTOS; TYRK, I.
PROSTIE; PSOMOTOS; TYRK NGER, I.
KINAGE, TYRK, I.
PROSTIE; PSOMOTOS; TANTE NGER, I. UNKNOWN I.
KINAGE; TYRE NGER, I. UNKNOWN I.
KINAGE; TYRE NGER, I. NON TER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1232 DPPERGAPPSTFKGTPTAENPEYLGL 1257
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01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCNEHCAGGCTGPRATDCLACRDFNDDGTCKDTCPP------PKIYDIVSHQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 VVDNPNIKYTFGAACVKECPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPK 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVF 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGH 525
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                                                                                                                                                                                                                                                                                                                                                                                      VLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 TSNPTMNLIPHAFERQCQKCDPGCVNGSCWAPGPGHCQKFTKLLCAEQCNRRCRGPKPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
                                                                                                                                                                                                                                           176 NNQLALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTD
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                                                                                                                                                                        Indels 162;
                                                                                                                                Length 1165;
PRÔSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 2.
PROSITE; PS00109; PROTEIN'KINASE TYR; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein Kinase.
SEQUENCE 1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                                                                                                                            Query Match 39.8%; Score 2724; DB 13; Best Local Similarity 45.5%; Pred. No. 5.6e-197; Matches 585; Conservative 160; Mismatches 379;
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-----KUNLPEKAKKAFDNPDYWNHSLPPRSTLQHPDYLQEYSTKYFYKQNGRIRPIVA 1108
 1004 VSRRKNGDLQAVDNPEYHN-----APNGQPKAEDEYVNEPLYLNTFANTLENAEYL-- 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 TYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 WGLLLALLPP--GAASTQ----VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WRLILMCVASRLRAASSQTQEAVCPGTQNGLSSTGSQENQYNLNKDRYKGCEIIMGNLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 LNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTGPKHSDCLACLHFNHSGICELHCP-ALVFNNFTVSFWLRVPKVSASHLERYTFGAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 AĞCKĞPLDTDCFACRLFNDSĞACVPQCPQTLIYNKQTF-----QMETNPNAKYQYĞSI
                                                                                                                                                                                                                                                                  Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1328;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99177347; PubMed=10077531;
Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA around the wntl locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1328 AA; 148613 MW; A333039258B647E9 CRC64;
                            QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGA--PPSTFKGTPT-
                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ErbB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
Local Similarity 40.3%; Pred. No. 1.3e-163;
es 521; Conservative 157; Mismatches 417;
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EMBL, AF056116; AAC34391.1; --
HSSP; P11362; 1FCK.

INTERPRO; 1PR000494; EGFR L domain.
INTERPRO; 1PR001919; EUK DKINASE.

INTERPRO; 1PR00174; FUITh-11ke.
INTERPRO; 1PR001245; Tyr Dkinase.
Pfam; PF00757; FUITH-11ke; I.

Pfam; PF00757; FUITH-11ke; I.

Pfam; PF001091; Recep L domain; 2.

ProDom; PD000001; EUK DKinase; 1.

SWART; SW00261; FU; 3, X NASE; SWART; SW00261; FU; SWART; SW00261; FU; S.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                     PRELIMINARY;
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SEQUENCE 1328 AA; 148
                                                                                    1250 ENPEYL 1255
                                                                                                              1109 ENPEYL 1114
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              26;
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                                                                                                AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCP-ALVFNNFTV
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              Gaps
              85;
              Indels
             Mismatches 351;
 Pred. No. 1.6e-195;
             538; Conservative 172;
46.98;
 Best Local Similarity
Matches 538; Conserv
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                                             AWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTH 479
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             CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQR-CEKCSKPCARVCYGLGMEHLREV
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                                    RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 GSLAFLPESFDGDPASNT-----APLQPEQLQVFETLEEITGYLYISAWPDSLPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 IAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASPGGLREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 CTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1433;
                                                                                                                                                                                                                                                                                                              "Cloning, expression and localisation of the Anopheles gambiae epidermal growth factor receptor."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ301655; CAC35008.1; -- HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1433 AA; 159585 MW; E3D9D88967724F07 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.4%; Score 2011.5; DB 5 32.5%; Pred. No. 6.1e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00190; CYTOCHROME C; UNKNOWN 4. PROSITE; PS00107; PROTEIN KINASE ATP; 1. PROSITE; PS00109; PROTEIN KINASE DOM; 1. PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IRR000145; CytC heme bind.
InterPro; IPR000149; EGFR_L domain.
InterPro; IPR000199; Euk pkinase.
InterPro; IPR000179; Euk pkinase.
InterPro; IPR0012174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00157; Furin-like; 1.
Pfam; PF00109; Prini-like; 1.
Pfam; PF00109; TyrKINASE.
ProDom; PF00109; TYRKINASE.
ProDom; PF00109; TYRKINASE.
ProDom; PF00109; TYRKINASE.
SWART; SW00219; TYRKINASE; 1.
SWART; SW00219; TYRKINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                             Lycett G.J.;
                                                                                                                                                                                                                                                                    STRAIN-SUA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGENVKI PVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLIGICLISTVQLVTQLM
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                      DQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVE
                                                                                                  SEIKKSSDHEVMVQKNRNATECHEEGMECSEQCSKAGCWGKGPEQCLECKNVKYKGKCLD
                                                                                                                                                                         ---SGVKPDLSYMPIWKFPD--
                                                                                                                                                                                                                                                                    556 TTKHAMNGTCINCHKTCVGCRGPRDTIAPDGCISCDKAIIGSDAKIERCLMKDESCPDGY
                                                                                                                                                                                                                                                                                                                                                                                                             688 IRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIP
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                                                                                                                                                   ECRVLOGLPREY - VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
                                                                                                                                                                                                                                                                                                                                              616 YSDYVLQEEGPLKQLSGKAVCRKCHPRCKKCTGYGFHEQFCQECTGYKKGEQCEDECPQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1217 BDDYLMP-TCQSQ----TPG----YMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1190 VFAFGGAVENPEYL-----TPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ELTYLPTHASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCTGPKHSDCLACLHFNHSGICELHCPALVFNNFTVSFWLRVPKVSASHLERYTFGAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99415951; Pubmed=10485918;
Doberty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER.2/nu receptor tyrosine kinase gene encodes a secreted autoinhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 419;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, 8717761; AAD5609.2; -
InterPro; IPR00494; EGFR.L domain.

InterPro; IPR002174; Furin-like.

Pfam; PF00757; Purin-like; 1.

Pfam; PF01030; Recep L domain; 1.

SMART; SM00261; FU; 1.

SEQUENCE 419 AA; 45472 MW; FECIBE34752D030C CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.9%; Score 1770.5;
85.0%; Pred. No. 1.7e
                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 65.0%
Matches 340; Conservative
   PRELIMINARY;
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Q8R2X1
ID Q8R2
AC Q8R2
DT 01-J
DT 01-J
DE Hypo
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634 197 693 253 313 813 373 873

753

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SMART; SM0019; TyrKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 729 AA; 80649 MW; 84D2F6914EFE1D63 CRC64;
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Last annotation update)
                                                                                                        Query Match 25.1%; Score 1720; DB 15; Best Local Similarity 54.8%; Pred. No. 2.5e-121; Matches 358; Conservative 75; Mismatches 118;
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MEDLINE=94201859; PubMed=8152791;

MEDLINE=94201859; PubMed=8152791;

MEDLINE=94201859; PubMed=8152791;

Johnsson A., Beug H.;

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Oncogene 9:1307-1320(1994).

EMBL: S69372; AACG0725:1; -.
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Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                           Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027080; AAH27080.1; -.
Hypothetical protein.
SEQUENCE 367 AA; 40163 MW; OBE03395F9E101B0 CRC64;
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Viruses, Retroid viruses, Retroviridae, Alpharetrovirus.
VCBI_TaxID=11950;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MR4-2002 (TrEMBLrel. 20, Last annotation update)
POLYPROTEIN.
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InterPro; IPR004028; Retro M.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
Pfam; PF02813; Retro M; I.
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LGLDVPV 367
                                                              SEQUENCE FROM N.A.
                                       NCBI_TaxID=10090;
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                                                                                        575 PONGSVICEGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
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MEDLINE=94203659; PubMed=8152791;
Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
                                                 102;
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
NCBI_TaxID=11950;
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Johnsson A., Beug H.;
Retroviral capture of c-erbB proto-oncogene sequences. rapid
"Retroviral capture of viral genomes carrying mutant v-erbB genes
different transforming capacities.";
Docogene 9:1307-1320(1994).
EMBL; 869372; AAG60727.1;
HSSP; P11362; IFGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.1%; Score 1718; DB 15; Length 567; Best Local Similarity 55.4%; Pred. No. 2.5e-121; Matches 357; Conservative 73; Mismatches 112; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAKTLSPGKNGVVKDVF------AFGGAVENPEYL 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TAMVQNQIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63390 MW; C6D9CBA7ADF725E1 CRC64;
                                                                                                                                                                                                                         InterPro; IPR00019; Euk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam, PF00069; pkinase; 1.
PRNINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase; 1.
SWART; SW0219; TyrKC; 1.
PR0SITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE TYP; 1.
PROSITE; PS00109; PROTEIN KINASE TYP; 1.
Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                     444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
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QBWYVO
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PRELIMINARY;

QBWYV0 QBWYV0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                895 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                955 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Gaps
                                                                                                                                                                                                                                                                                                                          Qin W.X., Zhao X.T.,
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.8%; Score 1697.5; DB 4; Length 412; 80.5%; Pred. No. 5.5e-120; ive 5; Mismatches 22; Indels 53;
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A wan D.F., Gu J.R.;

"Novel human cDNA clones with function of inhibiting cancer growth."

I growth."

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

E EMBL, AF318349, AAL55856.1;

E InterPro; IPR000719; EVL pkinase.

R InterPro; IPR000719; EVL pkinase.

R InterPro; IPR000419; YIP motif.

R Fam; PF00069; pkinase; 1.

R ProDom; PD000001; ENL pkinase; 1.

R ProDom; PD000001; ENL pkinase; 1.

R PROSITE; PS50011; EVK pkinase; 1.

R PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gag, v-erb-A, v-erb-B protein.
GAG, V-ERB-A, V-ERB-B.
Avian erythroblastosis virus.
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Best Local Similarity 80.51
Matches 330; Conservative
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                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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10 Q6
AC Q6
D7 01
D7 01
DE G8
OS GA
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24.1%; Score 1645; DB 15; 54.9%; Pred. No. 7.8e-116; ive 70; Mismatches 121;
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Matches 345, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----CHPECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 IEKCOESYLLAFEHYINYRKHNIPHFWSKLLMKVADLRMIGAYHASRFLHMKVECPTELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I PVAIKVLRENTS PKANKE I LDEAYVMAGVGS PYVSRLLGICLTS TVQLVTQLMPYGCLL
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                                                                                                                                                                                                                                                   No. 1 InterPro; 1 PR00019; Euk pkinase.

InterPro; 1 PR00019; Euk pkinase.

InterPro; 1 PR000136; Hormone_rec_lig.

InterPro; 1 PR001125; Stdhrmn receptor.

InterPro; 1 PR001125; Stdhrmn receptor.

InterPro; 1 PR001125; Jry pkinase.

InterPro; 1 PR00164; Jry pkinase.

InterPro; 1 PR00169; Zf-C4; 1.

Prom; PR00105; Zf-C4; 1.

Rem; PF000069; pkinase; 1.

Rem; PF000001; Euk pkinase; 1.

Robom; PD000001; Euk pkinase; 1.

Robom; PD000001; Euk pkinase; 1.

Robom; PD000019; JryrKc; 1.

Robom; PD000019; TryrKc; 1.

Robom; PR0019; TryrKc; 1.

Robom; PR0019; TryrKc; 1.

Robom; PR0019; PR0TEIN_KINASE_ATP; 1.

RR PROSITE; PS00107; PR0TEIN_KINASE_ATP; 1.

RR PROSITE; PS00109; PR0TEIN_KINASE_TYR; 1.

RR PROSITE; PS00109; PR0TEIN_KINASE_TYR; 1.

RR ATP-binding; DNA-binding; Nuclear protein; Receptor;

Transcription regulation; Transferase; Tyrosine-protein kinase;
                                                                     24.2%; Score 1653.5; DB 15; Length 962; 51.7%; Pred. No. 4.1e-116; ative 73; Mismatches 142; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
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Retroviridae; Avian type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 VEECRVLQGLPRE-YVNAR-HCLP------
Retroid viruses;
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                   NCBI_TaxID=11861;
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1112
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994 VIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHR 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.;
"Common site of mutation in the erbB gene of avian erythroblastosis
"Common site of mutation in the erbB gene of avian erythroblastosis
"Common site of mutation in the erbB gene of avian erythroblastosis
"Common site of mutation in the erbB gene of avian erythroblastosis
"Common site of mutation in the erbB gene of avian erythroblastosis
"Common site of mutation in the erbB gene of avian erythroblastosis
"Nonger Res 1.265-278(1987).
"EMBL; X06943; CAA30024.1, Full pkinase.
"InterPro; IPR001245; Tyr pkinase.
"InterPro; IPR001245; Tyr pkinase.
"Probom PD0000091; Buk pkinase; 1.
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                                                                                                                                                                     867 -NSPST------SRTPLLSSLSATSN-----NSATKCIDRNGGH--
                                                                                                                                                                                                                               1113 SPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT
                                                                                                                                                                                                                                                              584 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-erbB gene.
Avian erythroblastosis virus.
Viruses; Retriod viruses; Retriod viruses; Retriod viruses; Retriodicity (Viruses)
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SMART; SM0219; TYTES 1.

PROSITE; PS001107; PROTEIN KINASE ATP; 1.

PROSITE; PS00111; PROTEIN KINASE TOM; 1.

ATP-Dinding; Transferase; Tyrosine-protein kinase.

PROSITE; PS0189; PROTEIN KINASE TOM; 1.

ATP-Dinding; Transferase; Tyrosine-protein kinase.

PROFITE 545 AA; 60899 MW; 140DCE8CCA0F8AF4 CRC64;
                           822 VIQGDERMHLPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFF
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InterPro; IRR000494; EGFR L domain.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
                                                                                                                                                                                                                                 EMBL; AF124513; AAD44149.1; --
EMBL, AF275366; AAC28047.1; --
EMBL; AF275364; AAC28047.1; JOINED.
EMBL; AF275365; AAC28047.1; JOINED.
                                                                                                                                                                                                                                                                                                                            EMBL, AKO04944, BAB23688.1) - EMBL, AKO04983, BAB23641.1; - EMBL, AKO04911, BAB23662.1; - MGD; MGI:95294; Egfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00261; FU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor.
SEQUENCE
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                                                                                    KGERLPOPPICTIDVYMIMVKCMMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG 1001
                                                                                                                                                                                    PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1061
                                                                                                                                                                                                                                                                             GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1116
                                                                                                                                                                                                                                                                                                                                                                         1117 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1175
942
                      STRAIN=C57BL/6J; TISSUE=LIVER;
STRAIN=C57BL/6J; TISSUE=LIVER;
STRAIN=C57BL/6J; TISSUE=LIVER;
Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Shibata K., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kauukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
YHADGGKVP1 KWMALES1 LRRRFTHQSDVWSYGVTVWELMTFGAKPYDG1 PARE1 PDLLE
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
Maihle N.J.;
"Alternative Transcripts from the Human and Mouse EGFR Genes Encode
Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamtya M., Lee N.H., Lyons P., Marchionni L., Mashima D., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., "
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Human heregulin 2
Human tyrosine kin
HER2 transgene pla
Human HER2 (ErbB2)
Human HER-2/neu on
Human HER-2/neu pr
Amino acid sequenc
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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13	6702	98.	2	23	AAM51143	
14	6702	98	25	23	AAU77114	Human Her-2/neu po
15	6629		43	14	AAR39568	-
16	6538		22	23	AAU98923	Human breast cance
17	6385		20	21	AAB21208	Human HER-2/neu pr
18	5905.5	98	25	21	•	Rat HER-2/neu prot
. 19	5905.5	. 98	1256	23	AAM51144	Rat Her-2/neu onco
20	5881.5	86.	25	21	AAB21206	Mouse Her-2/neu pr
21	5881.5	98	25	22	AAG62860	acid seque
22	5881.5	. 98	25	23	AAM51151	Her-
23	4788	70.	919	21	AAB21203	Human HER-2/neu fu
24	4788	70.	919	23	AAM51148	Her-2/neu extracel
25	4031.5	58.	920	23	AAM51152	Mouse Her-2/neu ex
56	4031.5	58.	926	23	AAM51153	Mouse Her-2/neu ex
27	3672	53.	712	21	AAB21204	Human HER-2/neu fu
28	3672	53	712	23	AAM51149	Her-2/neu extracel
29	3526	51.	782	18	AAW19764	Her2-GM-CSF immuno
30	3524	51.	653	21	AAB21200	Extracellular HER-
31	3524	51.	653	23	AAM51145	Human Her-2/neu on
32	3486	51.	645	22	AAB60408	Human ErbB2 oncopr
33	3486	51.0	645	22	AAB61593	ErbB2
34	3421	50.	951	21	AAY44993	DC8scFv-erbB2EC fu
35	3318		624	11	AAR08222	Extracellular port
36	3116	45.	21	21	AAB19259	Amino acid sequenc
37	3116	45.	21	21	AAY50616	Human EGF receptor
38	3116	45.	21	23	AAE23019	Human Her-1 protei
39	3116	45	1210	23	AAM50768	
40	3114	45.	21	22	AAB68420	acid seque
41	3084		583	23	AAE20483	Human protein for
42	3084		587	23	AAE20481	Human protein for
43	3083	45	589	23	48	Human protein for
44	3083	4	009	23	AAE20482	Human protein for
45	3075	45	1210	23		Human epidermal gr
					ALIGNMENTS	
RESULT 1						
AAY92620 ID AAY	92620	AAY92620 ID AAY92620 standard: Protein: 1255 AA	Prote		1255 AA	

Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer; cell-associated peptide antigen; foreign epitope. 59..73 /label= insertion_region /note= "sultable for foreign epitope insertion" 103...17 |/label= insertion region |/note= "suitable For foreign epitope insertion" 5..25 /label= insertion region /note= "suitable For foreign epitope insertion" /note= "mature polypeptide" AAY92620 standard; Protein; 1255 AA. Location/Qualifiers |..173 |label= N-terminal (first entry) Human heregulin 2 (Her2). Homo sapiens 10-AUG-2000 AAY92620; Key Domain Region Region Region

149..163 /label= insertion region /note= "suitable For foreign epitope insertion" 174..323

Region

Domain

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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the inscrtion of foreign T helper epitopes were identified (see features table). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dalum I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor associated prostate cancer
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/label= insertion_region
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note= "suitable for foreign epitope insertion'
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                                                                                                                                                                                                                                                                                                                555. 1010
/label= Tyrosine_kinase_domain
                                                                     124..483
|Tabel= Ligand_binding_domain
 label = Cysteine_rich_domain
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is used for inducing immune responses against weakly immunogenic cell-associated poptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 Pcroup derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate/Dreast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducting an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polywucleotides that encode peptides of the invention are useful as hybridisation probes and as primars for the detection of genes of gene transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polymucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
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/note= "Antigenic epitope"
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                                                                                             The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid particular, the antibody is directed against ErbB2 (also known as HER and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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                                    Treating tumors, particularly breast cancers, which overexpress ar receptor and does not respond to an anti-ErbB antibody, comprises conjugating the antibody to a maytansinoid -
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                                                                                                                                                                                   Query Match 98.1%; Score 6708; DB 22; Best Local Similarity 98.5%; Pred. No. 0; Matches 1242; Conservative 2; Mismatches 11;
                                                                            Example 3; Fig 4; 92pp; English.
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LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM 774
                                                                                             LAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCS
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(SCHW/) SCHWALL R.
(SLIW/) SLIWKOWSKI M.
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                                                                                                                                                                                                                                              The invention relates to treating a tumour in a mammal, where the tumour is characterised by the overexpression of an epidermal growth factor exceptor (ExbB) and does not respond or responds poorly, to treatment with an anti-ExbB antibody, comprising administering to the mammal an anti-ExbB antibody, comprising administering to the mammal an anti-ExbB antibody maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, balivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer cancer which overexpresses ExbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2)
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                                                                                                            Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
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Pred. No. 0;
2; Mismatches 11;
Σ
Sliwkowski
                                                                                                                                                                                                            English.
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Best Local Similarity 98.5%;
Matches 1242; Conservative 2
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Schwall R,
                                           2002-163686/21
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                                                                                                                                                                                                  Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, overian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
                                                                                                                              encoding HER-2-neu poly:peptide(s) - used for prevention or ntment of malignancies with which the HER-2/neu oncogene is
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Best Local Similarity 98.3%; Pred. No. 0;
Matches 1240; Conservative 3; Mismatches 12;
                                                                                                                                                                             Claim 2; Page 56-61; 71pp; English
                        95US-0414417
                                                WASHINGTON
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                                                                                             WPI; 1996-455361/45.
N-PSDB; AAT40739.
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LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI
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                                    VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
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676..1255
/label= Intracellular_domain
/note= "claimed domain, useful for immunisation"
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breast cancer; ovary cancer; colon cancer; lung cancer;
prostate cancer; immunisation; tumour; vaccine; vector.
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This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELTYLPTNASLSFLODIOEVOGYVLIAHNOVRQVPLORLRIVRGTQLFEDNYALAVLDNG
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                                                                                                                                                       Use of HER-2/neu polypeptides - for eliciting an immune response an HER-2/neu associated malignancy, particularly for treating or preventing tumours
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                                                                                                                                                                                                                                                                                                                                                               Length 1255;
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                                                                                                                                                                                                                                                                                                                                                           Score 6702; DB 20;
Pred. No. 0;
3; Mismatches 12;
                                                                                                                                                                                                           Claim 3; Column 31-38; 26pp; English
                                                                                                                                                                                                                                                                                                                                                          Query Match 98.0%;
Best Local Similarity 98.3%;
Matches 1240; Conservative 3
            96US-0625101.
93US-0033644.
93US-0106112.
95US-0414417.
                                                                          WASHINGTON
                                                                                                 Disis ML,
                                                                                                                         WPI; 1999-152835/13.
N-PSDB; AAX01912.
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            01-APR-1996;
17-MAR-1993;
12-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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for vaccinating against breast, ovarian, colon, lung and
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(CORI-) CORIXA CORP.
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                                                                                                                                                                                                 The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cystein residues, compared to the unspliced protein. The erbB-2 polymucleoride is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                                                                                                     Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
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                                                                                                                                                                     Claim 3; Fig 2; 60pp; English
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Matches 1240; Conservative
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                                     Muller WJ, Siegel PM
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                                                                                                                 LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor cell proliferation; tissue degeneration; arthropathy;
bone resorption; inflammatory disease; degenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the SPLICE erbB-2 receptor protein.
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The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as pl85 or c-erbB2).
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                                                                                               New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
              MVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDM
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The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cyctoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (I), bound to a channel elekocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino caids that have look identity with a native peptide sequence of HER2/neu; (2) a vaccine composition (III) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I); and (5) an isolated nucleic acid encoding (II) in as cytostatic and immunostimulant activities, and can be used in vaccines (I); (II) and (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (III) are useful for concision of cancer. (I) and (II) are useful for cancer. (I) and (III) are useful for conting or evaluating an immune response to a tumour-associated attigen when incubated with a T lymphocyte semple form a patient and detecting the presence of bound T lymphocyte to (I) or (II). Epitope cantigen when incubated with a T lymphocyte to (I) or (II). Epitope conting an unique may be avoided. Selected epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined from conting the ability to direct and focus an immune response to multiple tumour-associated and percent antigen is eliminated. The vaccine selected antigens from the same pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine conting the problem of tumour vaciality and reducing the likelihood of tumour vaciality and reducing the likelihood of tumour escape due to antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in the exemplification of the present invention.
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              An isolated prepared HER2/neu epitope useful in a vaccine for
cellular immune responses for the prevention and treatment of
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Best Local Similarity 98.3%;
Matches 1240; Conservative
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                       FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
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                                                                                                                                                                                                                                           The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
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                                                                                                                               Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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98.3%; Pred. No. 0;
ive 3; Mismatches
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for the therapy and diagnosis of cancer. I be composition is useful for the therapy and diagnosis of cancer. The compositions is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for the ther-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to caller the form duplex molecules with complementary stretches of the centire Her-2/Neu gene or gene fragments of interest, to isolate a full centified the suitable library, and to direct expression of a copypeptide in appropriate host cells. The composition is useful in corpophylactic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu corposition is useful in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                                                                                                                                             Novel isolated Her-2/Neu polypeptide composition useful for therapy prevention and diagnosis of cancer, preferably breast cancer
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                                                                                                                                            Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; Length 1255;
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Pred. No. 0;
3; Mismatches 12; Indels
                                                                                                                                            Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is human Her-2/neu protein.
                                                                                                                                            Foy TM,
                                                                                                                                                                                                                                                                        Disclosure; Page 114-117; 129pp; English.
                                                                                                                                          Hand-zimmermann S, Cheever MA,
Mcneill PD, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.3%;
Matches 1240; Conservative 3
                                                       14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
                              14-AUG-2001; 2001WO-US41733
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                                                                                                                 (CORI-) CORIXA CORP
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N-PSDB; AAD32743
  21-FEB-2002
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1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
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1015 GDLVDAEEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGDLTLGLEPSEEEAPRSP
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                                                                                                                                                                     AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ1AKGMS
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                                                                                                                                                                                                                                                                   YLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESI
                                                                                                                                                                                                                                                                                 LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI
                                                                                                                                                                                                                                                                                                                                       MVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDM
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                                                         FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
                                                                                               VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
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                                         FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
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human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
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The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its coveragession correlates with a poor prognosis in breast and overexpression correlates with a poor prognosis in breast and coveragession correlates with a poor prognosis. In breast and vaccines overing the fusion proteins or nucleic acid molecules. In proteins, nucleic acids encoding them, viral vectors, and vaccines comprishing the fusion proteins or nucleic acid molecules. In preferred fusion proteins the extracellular domain or protein is fused to a Her-2/neu intracellular domain or protein is fused to a Her-2/neu intracellular domain or protein is fused to a Her-2/neu intracellular domain or protein is elicited or enhanced by transfecting cells of an animal ex vivo with a nucleic acid condinistering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid concerned specially breast, ovarian, colon, lung or prostate cancer concerned the fusion protein in the development of a cancer, specially breast, ovarian, colon, lung or prostate cancer in a patient. I cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in corder to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
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Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
tyrosine kinase; receptor; c-erbB2; gene therapy.
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3; Mismatches 12; Indels
                                                                                                                                                                                  /note= "phosphorylation domain"
                                                                                                              /note= "extracellular domain"
676.1255
/note= "intracellular domain"
990.1255
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                              Location/Qualifiers
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Best Local Similarity 98.3
Matches 1240; Conservative
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                                                  Homo sapiens
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35 AVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISA 414
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                                                                                                481 CFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
                                                                                                                   CFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGFTQCVNCSQF
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Best Local Similarity 98.3%;
Matches 1240; Conservative 3
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28-SEP-2000; 2000US-0675904.
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                                                                                       CLL;
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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                                                                                                                                                                                       c-erbB-2; glycoprotein
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                                                                                                                                                                      c-erbB-2 tumour antigen.
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                                                                                                                  Protein; 1433
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N-PSDB; AAQ46083.
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Best Local Similarity
Matches 1233; Conserv
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                                                                                               AAGCTGPKHSDCLACLHFNHSGICELHCPALVFNNFTVSFWLRVPKVSASHLERYTFGAS
                                                                                                          CFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
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                           DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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Search completed: July 22, 2003, 08:41:06 Job time : 43.1589 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model OM protein July 22, 2003, 08:25:54; Search time 23.0157 Seconds (without alignments) 5267.077 Million cell updates/sec Run on:

SEQ4-325-339-14 6852

1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 Total number of hits satisfying chosen parameters: 283224 segs, 96134422 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	7 or increase the desired	profein-tvrogine k	p-185 precursor -	epidermal growth f				>	kinase-related tra	epidermal growth f	rosine	protein-tyrosine k			lated tr	Drotein-tyrogine k		epidermal growth f	et-23 [i			growth	growth		Vrogine		3	insulin receptor o	-like grow
SUMMERIES	ID	A24571	TVRTNU	148161	GOHUE	A53183	TVCHLV	A47253	S06142	A36223	JC4387	TVFVLV	TVYUH	S35745	GOFFE	S00727	B44776	TVFVEB	A36325	E88257	S70712	S70713	A45558	A42032	A27131	S13807	S13808	T43220	INHUR	T43212
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	Query Match	98.2	86.5	86.3	46.0	45.6	45.2	43.5		35.5	34.2	25.8	24.9	24.0	24.0	23.9	23.7	23.7	22.1	19.0	19.0	17.7	17.2	16.5	•	11.8	11.0	10.7	10.2	10.1
	Score	9	5925	5916.5	3150	3123	660	2981.5	2672	2430.5	2342.5	1766.5	1703	1647	1643.5	1640	1623	1621	1515	1300	1300	1214	1180	m	88	9	54	730	698	693
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ALIGNMENTS

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protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
NALetranate names c-reb-2 protein precursor; kinase-related transforming protein erb
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
R;Accession: AA55431; AA5481; A44188; B44188; I59509; I57622
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
Nature 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth
A;Reference number: A24571; MUID:86118663; PMID:3003577

A;Molecule type: mRNA A;Residues: 1-1255 cYAM> A;Cross-references: GB:X03363; NID:g211197; PIDN:CAA27060.1; PID:g31198 A;Cross-references: GB:X03363; NID:g4911197; PIDN:CAA27060.1; PID:g31198 R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985 A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epider

A;Accession: A25491

A; Molecule type: DNA A; Residues: 737-1031 <SEM>

A.Cross-references: (B:M11767; NID:g182163; PIDN:AAA15808.1; PID:g551282
R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromo A;Reference number: A44188; MUID:86070181; PMID:2999974
A;Accession: A44188
A;Residues: 740-910 <COUI>A;Residues: 740-910 <COUI>A;Coss-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989

A; Accession: B4188

A; Molecule type: mRNA
A; Recession: 1-517, "ALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 < COU2>
A; Molecule type: mRNA
A; Residues: 1-517, "ARLL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 < COU2>
A; Cross-references: GB: M11730; NID: 9183966

R; King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A; Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A; Reference number: 159509; MUJD: 85272597; PMID: 2992089

A;Status: translated from GB/EMBL/DDBJ

A Molecule type: DNA
A; Residues: 832-909 <REX>
A; Residues: 832-909 <REX>
A; Residues: 832-909 <REX>
A; Cross-references: GB:L23995; NID:9459807; PIDN:AAA15809.1; PID:9459808
B; Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A; Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptions
A; Reference number: I57622; MUID:87286898; PMID:3039351

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <TAL>

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A;Molecule type: mRNA
A;Residues: 1-1260 «BAR»
A;Cross-references: EMBL:X03362; NID:956745; PIDN:CAA27059.1; PID:956746
A;Cross-references: EMBL:X03362; NID:956745; PIDN:CAA27059.1; PID:956746
B;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no
2-thiazoly1]formamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
C;Accession: A24562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related 1
A;Reference number: A24562; MUID:86118662; PMID:3945311
                                                                                                                                                                                                                                            780 MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM
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A;Note: authors translated the codon GCA for residue 25
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A;Cross-references: GB:M16792; NID:918393; PIDN:AAA58637.1; PID:9553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 36
C;Genetics:
C;Genetics:
A;Gene: GDB:RBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Map position: 19741.1.179721.1
A;Map position: 19741.1.179721.1
A;Matcons: 25/1; 75/3; 14771; 883/3
A;Note: the list of introns is incomplete
C;Function: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein; phosphoprotein; phosphorylation; autophosphorylation; duplication; glycoprotein; phosphorylation; catalyzes the status predicted <SIG>F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>F;22-653/Domain: signal sequence #status predicted <EXT>F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <ATM>F;22-653/Domain: EGF receptor extracellular domain repeat <EB2>F;22-1255/Domain: EGF receptor extracellular domain repeat <EB2>F;22-653/Domain: EGF receptor extracellular domain repeat <EB2>F;24-675/Domain: protein kinase ATP-binding motif F;651-234/Region: protein kinase ATP-binding motif F;686/Binding site: phosphate (Thr) (covalent) kinase C) #status predicted F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F;686/Binding site: phosphate (Tyr) (covalent) (by protein kinase C) #status predicted F;686/Binding site: phosphate (Tyr) (covalent) (by protein kinase C) #status predicted F;686/Binding site: phosphate (Tyr)
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Pred. No. 1.6e-267;
8; Mismatches 4;
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Best Local Similarity 98.4%;
Matches 1242; Conservative 8
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p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
                                                                                                                                                1017 DDWGDLVDAEEYLVPQQGFFSPDPTPGTGSTAHRRHSSSTRSGGGELTLGLEPSEEGPP 1076
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    ESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDV
                                                                                                   957 YMIWVKCWIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPSSPMDSTFYRSLLED
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1254 <RES>
A;Cross-references: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID:g747595
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: epidermal growth factor receptor; protein kinase C;Keywords: ATP F;718-983/Domain: protein kinase homology <KIN> F;726-734/Region: protein kinase ATP-binding motif
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86.3%; Pred. No. 2.4e-234;
tive 66; Mismatches 98;
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Matches 1089; Conserv
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Best Local Similarity 86.6%; Pred. No. 1.1e-234;
Matches 1095; Conservative 56; Mismatches 103; Indels
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                                      LCEVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQ
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                           YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMFNNFTVSFWLRVP
                                                                   K-VSASHLEEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYIS
                                                                                                          AWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTH
                                                                                                                       FLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDP
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N; Contains; protein-tyrosine kinase (EC 2.7.1.112) erbB

N; Contains; protein-tyrosine kinase (EC 2.7.1.112) erbB

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Species: Homo sapiens

C; Species: Homo spiens

C; Species: Homo spiens

A; Mclescule type: Man

A; Molecule type: Man

A; Molecule type: Mall: X00588; NID: 331113; PIDN: CAA35240.1; PID: G757924

A; Molecule type: Mall: Acad. Sci. U.S. A. 82, 4920-4924, 1985

A; Molecule type: Mall: Acad. Sci. U.S. A. 82, 4920-4924, 1985

A; Molecule type: Mall: Acad. Sci. U.S. A. 82, 4920-4924, 1985

A; Molecule type: DNA

A; Accession: A25772

A; Multile: Characterization and sequence of the promoter region of the human epidermal graph center type: DNA

A; Accession: A25772

A; Multile, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.

A; Accession: A2572

R; Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.

A; Accession: S30024; MUID: 88217333; PMID: 3329716

A; Meleidues type: DNA

A; Molecule type: DNA
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A./Cross-references: EMBL.X06370; NID:931118; PIDN:CAA29668.1; PID:931119
B.Hidley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1755, 1991
A.Title: Contributory effects of de Novo transcription and premature transcript termine
A./Accession: A38672; MUID:91107677; PMID:1988448
A./Accession: A38672; MUID:91107677; PMID:1988448
A./Accession: A38672; MUID:91107677; PMID:1988448
A./Accession: A38672; MUID:91107677; PMID:AA3171.1; PID:9553271
A./Accession: A06810; J84
A./Title: Human epidermal growth factor receptor CDNA is homologous to a variety of RNAs, A./Accession: A06810; J84
A./Title: Human epidermal growth factor receptor CDNA is homologous to a variety of RNAs, A./Accession: A00642; MUID:84245835; PMID:6330563
A./Accession: A00642
A./Accession: A00642
A./Accession: A00642
A./Accession: A041049
A./Title: Expression cloning of human carcinoma cells, which have large numbers of EGF receptor Complementary DNA: gene amplification A./Accession: A43615; MUID:84196372; PMID:6326261
A./Accession: A13-964 4.M.
A./Accession: A43-048
A./
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A;Accession: A05281
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A;Residues: 25-30,'S',32-51;454-467
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WMIDSECRPRFRELVSEFSRWARDPORFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDL 1023
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             LHAFENLEIIRGRTKQHGQFSLAVVSLNITSLGLRSLKEISDGDVIISGNKNLCYANTIN 476
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R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208
A;Title: Identification of residues in the nucleotide binding site of the epidermal grow A;Accession: A60143
A;Molecule (type: protein
A;Molecule (type: protein
A;Residues: 740-744, X', 746-747
A;Reference number: A38023; MUID:84191554; PMID:6125948
A;Title: ATP-stimulated interaction between epidermal growth factor receptor and superce A;Reference number: A38023; MUID:84191554; PMID:6125948
A;Contents: annotation; receptor activity
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.
A;Reference number: A33313, MUID:90003233; PMID:2790960
A;Contents: annotation; internalization signal
C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor C;Genetics:
A;Gene: GDB:EGFR
                                                                                                                                                                                                                                                                                                                                                                                                    A/Cross-references: GDB:120610; OMIM:131550

A/Map position: 7p12.3-7p12.1

A/Map position: 7p12.3-7p12.1

A/Map position: 7p12.3-7p12.1

A/Map position: 7p12.3-7p12.1

C/Superfamily: epidermal growth factor receptor; protein kinase homology

C/Superfamily: epidermal growth factor receptor; protein; phosphoprotein; phosphoprotein; phosphoprotein; proposition; and sequence #status predicted <AMT>
F:12-4/Domain: store receptor #status predicted <AMT>
F:25-1200/Domain: EGF receptor extracellular domain repeat <EE1>
F:390-600/Domain: EGF receptor extracellular domain repeat <EE2>
F:490-600/Domain: Intracellular #status predicted <1MT>
F:400-700/Domain: protein kinase homology <KIN>
F:710-975/Domain: protein kinase homology <KIN>
F:710-75/Domain: protein kinase ATP-binding motif
F:999-1046/Region: coated-pit mediated internalization signal
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46.0%; Score 3150; DB 1; Length 1210;
Best Local Similarity 49.6%; Pred. No. 1.7e-121;
Matches 631; Conservative 178; Mismatches 350; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:128,175,352,413,444,528,603/Binding site: carbohydrate (Asn)
F:745/Active site: Lys #status experimental
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1198 ENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPP 1240
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                                                                                                                                                                                                LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM 780
                                                                                                                                                                                                                                                                                                                              FVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFL 541
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                                                                                                    LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGM--FNNFTVSFWLRVPK 361
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                                                      RGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPF
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                                CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                             VSASHLEEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAW
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|GIFKG-PTAENAEYLRVAPP 1203
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RAVIVI, A.; Lax, I.; Ullitch, A.; Schlessinger, J.; Givol, D.; Moree, B.

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Ancession 6, 21,670, 191111, 191111, 1912266; PMID:201016

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 2.2-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A47253
R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.; I
Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HERA/p180erbB4, a fourth member of the epiderma.
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1089 SIDDGFL-----PAPEYVNQ--LMPKKPS----
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                                              Publication growth factor receptor precursor - chicken
Nicontains: procein-tyrosaine Kinase (EC 2.7.1.12) erbB
Nicotes: 2a-b2196 Hageluscoc revision 05-May-1995 #text_change 04-Feb-2000
C;Accession: A27720; Ano643
Nol. Cell Biol. 8, 1970-1978, 1988
Nol. Cell Piol. 8, 1970-1978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD
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Matches 630; Conservative 177; Mismatches 345; Indels 151; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.2%; Score 3099.5; DB 1; Length 1223; 48.3%; Pred. No. 1.9e-119;
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39.0%; Score 2672; DB 1; 44.9%; Pred. No. 5e-102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423
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                                                                                                                                                                                                                                                                                                                           NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI
                                                                                                                                                                                                                                                                                                                                                                                185 DINRSRACHPCSPMCKGSRCWGESSEDCOSLIRTVCAGGC-ARCKGPLPTDCCHEQCAAG
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                                                                                                                                                                                                                  WGLLLALLPPGAA----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTY
                                                                                                                                                                                          Gaps
            A;Accession: A47253
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-1308 -PLO>
A;Residues: protein Rinase homology conceptor; protein kinase homology
C;Reywords: AFP; growth factor receptor; protein kinase homology
F;716-981/Domain: protein kinase homology cKIN>
F;724-732/Region: protein kinase ATP-binding motif
                                                                                                                                                            43.5%; Score 2981.5; DB 2; Length 1308;
llarity 45.2%; Pred. No. 1.3e-114;
Conservative 187; Mismatches 375; Indels 179;
Reference number: A47253; MUID:93189574; PMID:8383326
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Best Local Simi
Matches 611;
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C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein;
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-1166/Product: Kinase-related transforming protein (Tu) #status predicted <MAT>
F;70-972/Domain: protein kinase homology <KIN>
F;715-723/Region: protein kinase ATP-binding motif
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                                                                                                                                                             942
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Cjate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000 G; Accession: S06142; S13809
Fivitherbordt, J., Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, Nature 341, 415-421, 1989
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-indu A; Reference number: S06142; MUD: 90015140; PMID: 2797166
                                                                                                                                                                                                                                                                  -----ENPFVSRR------KNGDLQ------ALDNPEYHNASNG----
                                                                                                 PIKWMALESILRRRFTHOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQP
                                                                                                                                  PICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIONED-LGPASPLDST
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                                                                                                                                                                                                                                                                                                                                                                                                  -----PLAP-SEGAGSDVFDGDLGMGA
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A;Molecule type: DNA
A;Residues: 821-1025, 'N',1027-1098,'A',1100-1166 <ADA>
A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
C;Genetics:
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A;Residues: 1-1166 <WIT>
A;Residues: 1-1166 <WIT>
A;Cross-references: EMBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291
R;Adam, D.; Maeueler, W.; Schartl, M.
Oncogene 6, 73-80, 1991
A;Title: Transcriptional activation of the melanoma inducing Xmrk oncoges
A;Reference number: S13807; MUID:91125882; PMID:1846957
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Matches	572; Conservative 171; Mismatches 385; Indels 146; Gaps 30;	
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Š i	AALCKWGELEALBERGAAAIQVCIGIDMKLKEPASFETHEDMLKHEYQGCQVVQQN	qq
q	8 AALLQLLLVLSISRCCSTDPDRKVCQGTSNQMTMLDNHYLKMKKMYSGCNVVLEN 62	È
ò	60 LELTYLPTNASLSFLQDIQEVQCYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119	\$ 6
QQ	63 LEITYTQENQDLSFLQSIQEVGGYVLIAMNEVSTIPLVNIARLIRGQNLYEGNFTLLVMSN 122	g 8
ò	120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179	Š i
qq	123 YQK-NPSSPDVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWWDIVDKTSNP 179	සු ,
ć	180 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE 238	ò
QQ	:	셤
ò	239 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA 298	RESULT
Q	240 HCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAACVKE 299	A36223 kinase-1
۵,	299 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMFN-NFTVSFWL 357	C; Specie C; Date:
ηq	VTE-G	R; Kraus,
λ̈	358 RVPKVSASHLEEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLY 417	A; Title
qq	355VNSTNIRSFSNCTKINGDIILNRNSFEGDPHYKIGTMDPEHLMNLTTVKEITGYLV 410	A; Retere
ò	418 ISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHH 476	A; Statue A; Molecu
QQ	411 IMMWPENMTSLSVFQNLEIIRGRTTFSRGFSFVVVQVRHLQWLGLRSLKEVSAGNVILKN 470	A; Kesidi A; Cross
ò	477 NTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVN 536	R; Plowms Proc. No
qq	471 TLQLRYANTINWRRLFRSEDQSIEYDARTENQTCNNECSEDGCW-PGPTMCVS 522	A;Title: A;Refere
ò	537 CSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHY 596	A; Access A; Status
οp	523 CLHVDRGGRCVASCNLLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGPQRANCSKSAHF 582	A;Resid
ò	597 KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP 656	A; Cross C; Geneti
Op	PRCPHGILGDGDTL-IWK	A; Cross
λ̈́o	657 LTSIVSAVVGILLVVVLGVVFGILIKRRQVKIRKYTMRRLLQETELVEPLTPSGAMPNQA 716	A, Map po
Ор	641 SSLAVGLVSGLLITVIVALLIVVLLRRRRIK-RKRTIRCLLQEKELVEPLTPSGQAPNQA 699	C; Keywor F; 707-97
ò	717 OMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDE 776	F; /15-72
QQ	700 FLRILKETEFKKDRVLGSGAFGTVYKGLMNPDGENIRIPVAIKVLREATSPKVNQEVLDE 759	Query Best I
ò	777 AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA 836	Marcine
q	760 AYVMASVDHPHVCRLLGICLTSAVQLVTQLMPYGCLLDYVRQHQERICGÓWLLNWCVQÍA 819) f
ò.		3 8
Q		6 6
è 6	897 LESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPFICTID 956	8 8
3 6	DESTRUCTIONS CAN STOAT AMERICA CONFIDCT FANELAS VEENGEREPUPPLITE	qq
è 8	95. VYMIUKKUMMIDSECRRRFRELVSEPSRMARPPORFVVIONEDLGPASPLDSTFYRSLLE 1016	ò
6	DDDMGDLVDAEEVLVPOXGEPCPDPAPGAGGMXHHPHPSGGGTGGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	qq
	SDDDVVDADEYLLPYKRI	ò
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us: preliminary
cule type: mRNA
dues: 1-1342 KRRA>
dues: 1-1342366
Breferences: GB:M29366
man, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G
Matl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
e: Molecular cloning and expression of another epidermal growth factor receptor-)
e: Molecular cloning and expression of another epidermal growth factor receptor-)
esion: IS9164
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sa-references: GDB:119880; OMIM:190151
position: 12q13-12q13
refamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homo.
ords: ATP; phosphotransferase
972/Domain: protein kinase homology «KIN»
723/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
e: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal
rence number: A36223; MUID:90083234; PMID:2687875
1077 PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVA 1135
                                                1020 --EPCIPPTGH---------PURENSITLRNISDPTQNALEKDLDGH-- 1055
                                                                                                                                              1136 PLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSPG 1182
                                                                                                                                                                                       1056 -----EYVNQPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNTN 1107
                                                                                                                                                                                                                                                                                        1183 KNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPST 1242
                                                                                                                                                                                                                                                                                                                                                           1108 QNSL---PLVSSGSMDDPDY---QAG-----YQAAF-----LPQTGALTGN 1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ies: Homo sapiens (man)
: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
ssion: A36223; IS9164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -related transforming protein (erbB3) (EC 2.7.1.-) precursor - human
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clube type: mRNA
dues: 1-559. (2', 561-957, 'F', 959-1063,'G', 1065-1342 <RES>
g_references: GB:MJ4309; NID:g183990; PIDN:AAA35979.1; PID:g306841
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VNGYVMPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDED-----EEYEYMNRRRRHS 1207
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                                                                                                                                                                                         RCPSGVKPDLSYMP1WKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA----SPLTSI
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                                                                                             PQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFV-V
                  DVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMFNNFTVSFWLRVPKVSASH
                                                  LEEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
                                                            DLSVFONLQVIRGRILHNGAYS-LTLQCLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
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                            1211 POPHPPPAFSPAFDNLYYWD
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A;Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue C;Comment: This protein is a functional heregulin receptor that transduces signals to th
                                                                                                                             characterization of the recombinant protein.
PMID:8522190
                                                                                                                                                                                                                                                                                                     C.Genetics:
A.Gene: BrbB3
A.Gene: BrbB3
A.Gene: BrbB3
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homo
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein; transmembrane protein
C.Keywords: Arp; growth factor receptor; liver; phosphoprotein; transmembrane fatatus predicted <SIG>
F;10-19/Domain: signal sequence #status predicted <SIG>
F;20-1339/Product: epidermal growth factor homolog #status predicted <TMM>
F;705-970/Domain: transmembrane #status predicted <TMM>
F;705-970/Domain: protein kinase homology <KIN>
F;713-721/Region: protein kinase ATP-binding motif
F;313-721/Region: protein kinase ATP-binding motif
F;313-711/Region: protein kinase ATP-binding motif
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                                                                                                S.L.; Koland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432; Indels
                                                                                                                                                                                       A;Molecule type: mRNA
A;Reaidues: 1-1339 <HEL>
A;Cross-references: GB:U29339; NID:g915389; PID:g915390
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.2%; Score 2342.5; DB 2;
ilarity 40.5%; Pred. No. 1.6e-88;
Conservative 174; Mismatches 432;
epidermal growth factor receptor homolog precursor - 1 N.Alternate names: ErbB3 protein; HER3 protein C.Species: Rattus norvegicus (Norway rat) C.Becies: 17-Jan-1996 #sequence_revision 19-Apr-1996 #te C.Accession: J64387 R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.I Gene 165, 279-284, 1995 A.Title: Cloning of the rat ErbB3 cDNA and characteriz A;Reference number: JC4387; MUID:96096535; PMID:852219 A;Accession: JC4387;
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10 RESULT JC4387

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A,Molecule type: DNA
A,Residues: 1-604 <YAM>
BENDALIA: B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Science 224, 1456-1459, 1984
A;Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new A,Reference number: A38022; MUID:84223957; PMID:6328658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1002 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPAFDNLYYWDQ------DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1260
                                                                                                                                    584 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                                                                                                                             DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                                                                                                                                                                                                VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
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                                                                                           125;
                                             Length 698;
                                                                                         80; Mismatches 137; Indels
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                                                                  .7e-65
                                             25.8%; Score 1766.5; 52.2%; Pred. No. 2.7e
      Lys #status predicted
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                                                                                           Conservative
                                                                  Best Local Similarity
Matches 374; Conserv
      F;229/Active site:
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N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase
C;Species: avian leukosis virus, ALV
C;Date: 31-Dec-1911 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999
C;Accession: B00643; A00643
E;Nilsen, T. W.; Maroney, P. A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.
Cell 41, 719-726, 1985
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and proformation: B00643; MUID:8528222; PMID:2988784
A;Reference number: A00643; MUID:8528222; PMID:2988784
A;Recession: B06643
A;Molecu.: type: mRNA
A;Resterence number: A00643; MUID:8528222; PMID:2988784
A;Resterence number: A00643; MUID:8528222; PMID:2988784
A;Resterence number: A00643
A;Molecu.: type: mRNA
A;Resterence number: A00643; MUID:8528222; PMID:2988784
A;Resterence number: A00643; MUID:8528222; PMID:2988789
F;10-6/Product: gag protein (fragment) #status predicted <AAGA:
F;60-698/Product: gag protein (fragment) #status predicted <AAGA:
F;10-4759/Domain: protein kinase ATP-binding motif
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                                                                                                                                                    LDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCM
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RDGPHCVNSCPHGILG--AKGPIYKYPDAQNECRPCHENCTQGCNGPELQDCLGQAEVLM
                                                                      | ::: | | | :| : | : | SKPHLVIAVTVG--LAVILMILGGSFLYWRGRRIQNKRAMRRYLERGESIEPLDPS-EKA
                                                                                                                                NQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEI
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A;Reference number: S15743
A;Accesabion: S15745
A;Accesabion: S15745
A;Accesabion: S15745
A;Accesare references: EMBL:X12707
C;Genetics:
A;Gene: exbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Reywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
F;135-400/Domain: protein kinase homology «KIN»
F;143-151/Region: protein kinase ATP-binding motif
F;170/Active site: Lys #status predicted
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A;Accession: A38022
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-28, W',30-139,'F',141-145,'V',147-152 <DEB>
A;Cose_references: GB:K02006
C;Genetics: erb
A;Gene: erb
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific;F;130-135/Donain: protein kinase homology <KIN>
F;130-135/Donain: protein kinase Arp-binding motif
F;138-146/Region: protein kinase Arp-binding motif
F;155/Active site: Lys #status predicted
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                                                                                                                                                                                                                               Indels 126;
                                                                                                                                                                                                  Length 604;
                                                                                                                                                                                              Query Match 24.9%; Score 1703; DB 1; 1
Best Local Similarity 52.2%; Pred. No. 9e-63;
Matches 360; Conservative 76; Mismatches 128;
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Opidermal growth factor receptor - fruit fly (Drosophila melanogaster)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Specials: Drosophila melanogaster
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1989
C;Accession: A00640; A38021
C;Accession: A00640; A38021
C;Accession: A00640; A38021
C;Accession: A; Shilo, B.Z.
C;Accession: Applease (BC A)
C;Accession: A; Shilo, B.Z.
C;Accession: A; Sepal, D.; Schlessinger, J.; Shilo, B.Z.
A; Title: The Drosophila EGF receptor gene homolog: conservation of both hormone bindin-A; Reference number: A00640; MUID: 85124611; PMID: 2982499
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                                                                                        GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
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                                                Gaps
                                             92;
24.0%; Score 1647; DB 2; Length 5:
54.9%; Pred. No. 1.6e-60;
ive 70; Mismatches 121; Indels
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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C;Species: avian erythroblastosis virus C;bace: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 R;Vennstroem, B.

RESULT 13

835745

submitted to the EMBL Data Library, March 1993

	H 80 H	A-RCKGPLPTDCCHEQCAGCTGPKHSDC 252	RESULTHHYTHLCFV 483
A;Accession: A00640 A;Molecule type: DNA A;Residues: 1.1330 A;Accession: Bill: K03054 R;Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D. A;Cross-references: EMBL: K03054 R;Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D. A;Arlitle: A Drosophila genomic sequence with homology to human epidermal growth A;Reference number: A38021; MUD:85137938; PMID:298323 A;Accession: A38021 A;Molecule type: DNA A;Residues: "A', 812-866, 'V', 868-943, 'QTPSLVK' <wad> A;Cross-references: EMBL: X02293; NID:97922; PIDN:CAA26157.1; PID:9929565 C;Comment: This sequence is tentative because the introns have not been ident C;Genetics: A;Gene: FlyBase:Egfr A;Cross-references: FlyBase:FBgn0003731 A;Map position: 2 57F C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: AFP; autophosphorylation; duplication; glycoprotein; phosphoprote F;733-764/Domain: intracellular #status predicted <twm> F;808-1072/Domain: protein kinase homology <kin> F;816-834/Region: protein kinase (Thr) (covalent) (by protein kinase C) #status F;843/Active site: Lys #status predicted F;1181/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status F;843/Active site: Lys #status predicted F;1181/Binding site: phosphate (Thr) (covalent) (by autophosphorylation)</kin></kin></kin></kin></kin></kin></kin></twm></wad>	Similarity 29.7%; Pred. No. 5. 2; Conservative 181; Mismatche VOGYVLIAHNQVRQVPLQRLRIVRGTQLF	195 CSPMCKGSRCWGESSEDCQSLTRTVCAGGC 195 CSPMCKGSRCWGESSEDCQSLTRTVCAGGC 142 CHESCTHG-CWGEGPRUCQKPSKLTCSPQC 253 LACLHFNHSGICELHCBALVTYNTDTFESM 1	Qy 425 LPDLSVPQNLQVIRGRILHNGAY-SITLQGLGISWLGLRSLRELGSGLALJHHNTHLCFV Db 361 FRNLSYFRNLETIHGRQLMESMPAALAIVKSSLYSLEMRNLKOISSGSVVIQHNRDLCXV QY 484 HTVPWDQLFRNPHQALLHTANRPEDEC

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1062 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLOSLPTHDPSPLQ 1116
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                                                                                                                                                            644 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
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C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; phosphotransferase F;135-400/Domain: protein kinase homology <KIN>F;143-151/Region: protein kinase ATP-binding motif
                                                           Query Match
23.9%; Score 1640; DB 2; Length 545;
Best Local Similarity 54.9%; Pred. No. 3e-60;
Matches 345; Conservative 69; Mismatches 122; Indels 92;
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Search completed: July 22, 2003, 09:09:31 Job time : 31.0157 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 22, 2003, 08:12:49; Search time 10.2304 Seconds (without alignments) 5088.033 Million cell updates/sec Run on:

SEQ4-103-117-12 6809 TFKGTPTAENPEYLGLDVPV 1255 Title: Perfect score: Sequence:

Scoring table:

112892 segs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		P04626 homo sapien	rattu	_	33	•	homod			P21860 homo sapien		P04412 drosophila		in	3 avian	_	8	P70424 mus musculu	9	P06213 homo sapien		_	4		ø	P14617 cavia porce	Q25197 hydra atten	P08069 homo sapien	'n		N	60		4
ID	:		ERB2_RAT	ERB2_MESAU	EGFR HUMAN	EGFR MOUSE	ERB4 HUMAN	ERB4 RAT	XMRK XIPMA	ERB3_HUMAN	ERB3 RAT	EGFR DROME	ERBB_ALV	ERBB AVIER	ERB# AVIEU	EGFR_CHICK	LT23 CAEEL	ERB2_MOUSE	ILPR BRALA	INSR_HUMAN	INSR_RAT	INSR_MOUSE	IRR_MOUSE	MIPR_LYMST	IRR_HUMAN	IRR_CAVPO	HTK7_HYDAT	IG1R_HUMAN	INSR AEDAE	IG1R MOUSE	IG1R_RAT	INSR_DROME	EPB4 HUMAN	EPB1_CHICK
% Query Match Length DB		1255 1	1257 1	1254 1	1210 1	1210 1	1308 1	1308 1	1167 1	1342 1	1339 1	1426 1	634 1	604 1	540 1	703 1	1323 1	245 1	1363 1	1382 1	1383 1	1372 1	1300 1	1607 1	1297 1	1300 1	1477 1	1367 1	1390 1	1373 1	1370 1	2146 1	987 1	984 1
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Q03145 mus musculu P07949 homo sapien	P54761 mus musculu P29317 homo sapien	P09759 rattus norv 091736 xenopus lae	P54762 homo sapien O91571 xenopus lae	Q00944 gallus gall	P53356 hydra atten P34152 mus musculu
EPA2 MOUSE RET HUMAN	EPB4 MOUSE EPA2 HUMAN	EPB1_RAT EPBB_XENLA	EPB1_HUMAN EPBA_XENLA	FAK1 CHICK FAK1 XENLA	HT16_HYDAT FAK1_MOUSE
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ALIGNMENTS

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                                                                                                                                                     AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140
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                                                                        LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILRRRFT
                                                                                  EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
       721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
                                        YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                                                                                           HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                                                                                                                                                                                                                                                           Bargmann C.I., Hung M.-C., Weinberg R.A., "The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erb8-2 precursor (EC 2.7.1.112)
(p185erb82) (NEU proto-oncogene) (C-erb8-2) (Epidermal growth factor receptor-related protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lai C., Lemke G.; "An extended family of protein-tyrosine kinase genes differentially
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D
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Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in the vertebrate nervous system.";
                                                                                                                                                                                                                                                                                                                                            PRT; 1257 AA
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TISSUE-Neuroblastoma;
MEDLINE-86118662; PubMed=3945311;
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MEDLINE=91222560; PubMed=2025425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.";
Nature 319:226-230(1986).
                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;

"Three dimensional structure of the transmembrane region of the proto-
cogenic and oncogenic forms of the new protein.";

EMBO J. 11:43-48(1992).

-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHY NEUREGULIN.

-!- FUNCTION: ESSENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
ALPHA AND AMPHIREGULIN.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.

-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.

-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.

-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB A HOMODIMER.

-!- SUBCLIULAR LOCATION: Type I membrane protein.

-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
RESIDUES (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE GGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KINASE ERBB-2.
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PROSITE; PS10109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE TOW; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR PROTEIN-TYROSINE EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Pfam; PF00757; Furin-like; I.
Pfam; PF01730; Recep L domain; 2.
Probom; PD00001; Euk Pkinase; I.
SMART; SM00261; FU; 3.
SMART; SM00219; TYKC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain.
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InterPro; IPR000494; BGFR L domain
InterPro; IPR000719; Buk pkinase.
InterPro; IPR00174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YuP motif.
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                                                                                                               FTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC
   SPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLMWCVQIAKGMSYLED
                                            VRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRR
                                 VRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMALESILRRR
                                                                          FTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC
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                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Last Sequence update)
15-JUN-2002 (Rel. 41, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(P185-EDB2) (NEU proto-oncogene) (C-erbB-2).
REBB2 OR NEU.
Mesocricetus auratus (Golden hamster).
Mesocricetus Actazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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15-DEC-1998 (Rel. 37, Last seq
15-JUN-2002 (Rel. 41, Last ann
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87.4%; Pred. No. 9.3e-313;
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AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP

LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC

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ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG

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YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN

AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTTCP

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DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 540

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ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL

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PROTEIN KINASE.
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                Probom; SM00261; Euk pkinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE TYR; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Transmembrane; Drosine-protein; Multigene family; Receptor; Signal; Transmembrane; Drosine-protein; Minase; ATP-binding; Phosphorylation; SIGNAL
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    http://www.isb-sib.
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Pred. No. 1.3e-311;
58; Mismatches 103; Indels
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  (See
entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                            EMBL, D16295; BAA03801.1;
HSSP; P11362; 1FGK.
InterPro; 1PR000049; EGFR L domain.
InterPro; 1PR000019; Euk pkinase.
InterPro; 1PR001014; Furin-like.
InterPro; 1PR001245; Tyr pkinase.
InterPro; 1PR001245; Tyr pkinase.
InterPro; 1PR004019; YLP motif.
Pfam; PF00157; Purin-like; 1.
Pfam; PF001030; Recep. L. domain; 2.
Pfam; PF02757; YLP; Z. L.
                                                                                                                    domain
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Best Local Similarity 87.1%;
Matches 1093; Conservative 56
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                     SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=84219729; PubMed=6328312;
WIlrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
Mayes E.L.V., Whittle N., Materfield M.D., Seeburg P.H.;
"Human epidermal growth factor receptor CDNA sequence and aberrant
expression of the amplified gene in A431 epidermoid carcinoma cells.";
                                                                         EGER HUMAN STANDARD; PRT; 1210 AA. P0653; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG5; Q92795; Q00732; Q00688; Q9BAS22; Q9H2C9; Q9GZX1; Q9H3C9; Q1-UUL-1986 (Rel. Q1, Created) (Rel. Q1, Created) (Rel. 35, Last sequence update) (Rel. 35, Last sequence update) Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor EGFR OR ERBB1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95382957, PubMed=7654168, Ilekis J.V., Stark B.C., Scoccia B.; Possible role of variant RNA transcripts in the regulation of epidermal growth factor receptor expression in human placenta.";
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TISSUE=Placenta;
MEDLINE=21100872; Pubmed=11161793;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland Balasubramaniam S., Croseley T.D., Magnuson T.R., James C.D.,
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Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M.,
Lampland.A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative genomic sequence analysis and isolation of human amouse alternative EGFR transcripts encoding truncated receptor
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MEDLINE=97256547; PubMed=9103388;
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SEQUENCE OF 1-29 FROM N.A.
MEDLINE=85270438; Pubmed=2991899;
IShii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;
"Characterization and sequence of the promoter region of the human epidermal growth factor receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
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Mroczkowski B., Mosig G., Cohen S.;
"ATP-stimulated interaction between epidermal growth factor receptor
and supercoiled DNA.";
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MEDLINE=85046483; PubMed=6093780;
Samen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G., O'Malley B.W.;
"Isolation of an evolutionarily conserved epidermal growth factor receptor cDNA from human A431 carcinoma cells.";
Biochem. Blophys. Res. Commun. 124:125-132(1984).
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Maihle N.J.;
"Human and mouse alternative EGFR transcripts encoding only the
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Haley J.D., Whittle N., Bennett P., Kinchington D., Ullrich A.,
Waterfield M.D.;
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Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., I Roe B.A., Merlino G.T., Pastan I.;
"Human epidermal growth factor receptor cDNA is homologous variety of RNAs overproduced in A431 carcinoma cells.";
Nature 309:806-810(1984).
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                                                                                                       extracellular domain of the receptor.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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96372; PubMed=6326261;
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SEQUENCE OF 1-29 FROM N.A.
MFD::TNE=91107677; PubMed=1988448;
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                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=98225196; PubMed=9556602;
Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
J. Biol. Chem. 273:11150-11157(1998).
                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                         Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D., "Characterization of the N-oligosaccharides attached to the atypical Asn-X-Cys sequence of recombinant human epidermal growth factor
                               MED'INE=96398132; PubMed=8962717;
Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;
"Analysis of the glycosylation patterns of the extracellular domain
the epidermal growth factor receptor expressed in Chinese hamster
overy fibroblasts.";
Growth Factors 13:121-132(1996).
    AND
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-!- ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (shown here), 2/p60/
truncated isoform/TEGFR, 3/p110 and 4; are produced by
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SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed in ovarian cancers.

-!- MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
    ASN-175; ASN-413; ASN-444
                                                                                                                                                                                  ASN-352; ASN-361; ASN-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Receptors for epidermal growth factor and other polypeptide
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TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is
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49.8%; Pred. No. 3.2e-162;
Live 176; Mismatches 353;
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CARBOHYDRATE-LINKAGE SITES ASN-128;
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CARBOHYDRATE-LINKAGE SITES ASN-56;
                                                                                                                                                                                                     ASN-603.
MEDLINE=20198209; Pubmed=10731668;
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EMBL, U95089; AAB53063.1; -...
EMBL, U48722; AAC50802.1; -...
EMBL, U48723; AAC50804.1; -...
EMBL, U48725; AAC50797.1; -...
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J. Bioche
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                                             308 VGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGC
                                                                                KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD
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          74 YDLSFLKTIQEVAGYVLJALNTVERIPLENLQIIRGNMYYENSYALAVLSNYD-
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68 73

106;

Indels

Conservative 176;

Similarity

Local

Best Loca Matches

630;

11

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Length 1210;

LLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN

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QPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TPQ 1200
                 1095 Q-SVPKRPAGSVQNPVYHNQPLNP-----APSRDPHYQD--PHSTAVGNPEYLNTVQ 1143
                                                           | : ||: ||
1144 ------PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGS-TAE 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eisinger D.P., Serrero G.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                               -----PERGAPPSTFKGTPTAE
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BALB/c, and CD-1; TISSUE=Liver, and Decidua;
MEDLINE=93186380; PubMed=7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B., "Comparison of EGF receptor sequences as a guide to study the ligand binding site.";
Oncogene 6:673-676(1991).
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=BALB/C; TISSUE=Liver;
Avivi A., Skorecki K., Yayon A., Givol D.;
Avivi A., Skorecki K., Yayon A., Givol D.;
Promoter region of the murine fibroblast growth factor receptor 2
(bek/KGFR) gene.";
Oncogene 7:1962(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The mouse waved-2 phenotype results from a point mutation in the receptor tyrosine kinase.";
Genes Dev. 8:399-413(1994).
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=B6/C3; TISSUE=Liver;
STRAIN=B6/C3; TISSUE=Liver;
MEDLINE=94170986. PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
EGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         PRT; 1210 AA.
                                             GGAAPQPHPPPAFSPAFDNLYYWDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-714 FROM N.A.
TISSUE=Brain;
MEDLINE=91232866; PubMed=2030916;
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                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                          1245 NPEYL 1249
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                        EGFR MOUSE
Q01279;
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              SÜBCELLULÂR LOCATION: Type I membrane protein.
MISCELLANBOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of cell DNA
synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00069; pkinase; 1.

Pfam; PF00057; Furin-like; 1.

Ream; PF00100; Recep L. domain; 2.

R Probom; Pp000001; Euk pkinase; 1.

R Probom; Pp00109; TyrKc; 1.

R SMART; SM00219; TyrKc; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

Transmembrane; Glycoprotein; Receptor; Signal; Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.

I SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
EPIDERMAL GROWTH FACTOR RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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PHOSPHORYLATION
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InterPro; IPR000494; EGFR. L domain
InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                  EMBL, X78987; CAASSS87.1; -.
EMBL, U03425; AAA17899.1; -.
EMBL, X59689; CAA42219.1; -.
EMBL, L06864; AAA53029.1; -.
EMBL, Z12608; CAA78249.1; -.
HSSP; P11362; 1FGK.
tyrosine phosphate
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MOD_RES
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Page 9

	1022 EYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGA	DD 1043 TSNPVPEY 1092 QY 1140 VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPCKNGVVKDVFAFGGAVENPEYL-T 1198	1199 POGGAAPQPHPPF	Oy 1243 AENPEYLGLDVP 1254 Db 1192 AENAEYLRVAPP 1203	25.4	AC Q15303; DT 15-DEC-1998 (Rel. 37, Created) DT 15-DEC-1998 (Rel. 37, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update)	Receptor protein-tyrosine kina (p180erbB4) (Tyrosine kinase-t ERBB4 OR HER4. Homo sapiens (Human).	Eukaryota; Me Mammalia; Eut NCBI_TaxID=96 {1}		'L., Neubauer M.G., Shoyab M.; gand'specific activation of HER4/p180erbB4, a fourth member of dermal growth factor receptor family "; oc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).	RN 12) RP SEQUENCE FROM N.A. (ISOFORMS JM-A AND JM-B), RC TISSUE-Fetal brain; RX MEDIJINS=97476287.	Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman (Klagsbrun M.; Khagsbrun M.; A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform	phorbol ester."; J. Biol. Chem. 272:26761
FT MOD_RES 1110 1110 PHOSPHORYLATION (AUTO-) (BY SIMILARITY). FT MOD_RES 1172 1172 PHOSPHORYLATION (AUTO-) (BY SIMILARITY). FT MOD_RES 1172 1172 PHOSPHORYLATION (AUTO-) (BY SIMILARITY). FT CARBOHYD 128 128 N.LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 175 175 N.LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 413 413 N.LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 528 N.LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 528 N.LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 528 S68 N.LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 603 603 N.LINKED (GLCNAC) (POTENTIAL). FT CONFLICT 539 539 C -> W (IN REF. 2). FT CONFLICT 991 991 L -> F (IN REF. 5). FT CONFLICT 1116 1117 HP -> PR (IN REF. 6). SEQUENCE 1210 AA; 134853 MW; 690E20P46DF2D2F5 CRC64;	Query Match Best Local Similarity 49.5%; Pred. No. 8.9e-161; Length 1210; Matches 630; Conservative 171; Mismatches 361; Indels 110; Gaps 23; Qy 11 LLLALLPPGAASTOVCTGTDWKLRLPASPETHLDMLRHLYQGGOVVQGNLELTYLPTN 68	Db 14 LLTALCAAGGALEEKKVCQGTSNRLTQLGFEDHFLSLQRNYNNCEVVLGNLFITTN 73 Oy 69 ASLSFLQDIQEVQSYVLIAHNQYRQVPLQRLRIYRGTQLFEDNYALAVLDNGDPLNNQYI 128 Db 74 YDLSFLKTIQEVAGYVLIALNTVBRIPLENLQIRGNALYENTYALALISN 124		QY 185 DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAG 243	OY 244 CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY 303	QY 304 LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQE 363 :	QY 364 FAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLYISAWPDSLPDLS 423	Qy 424 VFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD 483 Db 419 AFENLEIIRGRTKQHGQFSLAVVGLNITSLGLRSLKEISDGDVIISGNRNLCYANTINWK 478	OY 484 QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE 543 1 1 1 1 1 1 1 1 1 1	OY 544 CRVLQGLPREYVNARHCLPCHPECOPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSG 603 D	OY 604 VKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILL 663	Qy 664 VVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRK 722 1	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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R InterPro: IPR000195; Euk pkīnase.
R InterPro: IPR000174; Furin-like.
R InterPro: IPR0004019; Yurpin-like.
R InterPro: IPR001245; Yurpin-like.
R InterPro: IPR001245; Yurpinase.
R InterPro: IPR001245; Yurpinase.
R InterPro: IPR001245; Yurpinase.
R Pfam; PF00157; Furin-like; 1.
R Pfam; PF00157; Furin-like; 1.
R ProDom; PF001001; Euk_pkinase; 1.
R ProDom; PF001001; Euk_pkinase; 1.
R SMART; SM00261; FU; 4.
R SMART; SM00219; Tyrkc; 1.
R PROSITE; PS00110; PROTEIN KINASE ATP; 1.
R PROSITE; PS00110; PROTEIN KINASE DOM; 1.
R PROSITE; PS00111; PROTEIN KINASE DOM; 1.
R PROSITE; PS00111; PROTEIN KINASE DOM; 1.
R TARREFERSE; Tyrcoprocein; Multigene family; Receptor; Signal; Multigene family; Multigene family; Receptor; Signal; Multigene family; Multi
                                                                                                                                                                                                                                                                                                               SECEPTORS (POTENTIAL).

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM.A (SHOWN HERE) AND JM-B;

ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM.A (SHOWN HERE) AND JM-B;

ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN CRREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART. TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART, KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROLD, CEREBELLUM, LUNG, SALLVARY GLAND, AND PANCREAS.

PITULTARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS, LUNG, SALLVARY GLAND, AND PANCREAS.
FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, NRG-3. RRG-BING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF. TGF-A, AND AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4
                                                                                                                                                                                                                                       tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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 125 NOYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI
 179 STNGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPYVSDCCHRECAGG
 CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
 9 WGLLLALLPPGAA----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTY
 WVWVSLLVAAGTVQPSDSQSVCAGTENKLSSLSDLEQQYRALKKYYENCEVVMGNLEITS
 68 IEHNRDLSFLRSVREVTGYVLVALNQPRYLPLENLRIIRGTKLYEDRYALAIFLN----
 DINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG
 424 VFONLOVIRGRILHNGAYSLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD
 364 FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLS
 FINCTKINGNLIFLVTGIHGDPYNAIEAIDPEKLNVFRTVREITGFLNIOSWPPNMTDFS
 484 QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE
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 44.1%; Score 3003.5; DB 1; Length 1308;
 5E4AE80985D88761 CRC64;
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 1308 AA; 146807 MW;
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 EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEE 1069
 | | ...|| ::|| ::|| | ...|
1057 TPMSGNQFVYRDGGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCNGTLRKPVA 1116
 DEYVNEPLYLNTFANTLGKAEYLKONNILSMPEKAKKAFÖNPDYWNHSLPPRSTLQHPDYL 1259
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 LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 950
 CNLYDGEFREFENGSICVECDPQCEKMEDGLLTCHGPGPDNCTKCSHFKDGPNCVEKCPD
 TSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
 OMRILKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTSPKANKEILDE
 AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
 KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMA
 DEEDLEDMMDAEEYLVP-QAFNIPPP----IYTSRARIDSNRS----EIGHSPPPAY
 APRS------BLAP-SEGAGSDVFDGDLGMGAAKGLQS
 1101 LPTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPR
 ENPFVSRR------PPKAE
 --PAEQRASPL
 EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPA-
 ------PPSTF
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ERB4 RAT STANDARD; PRT; 1308 AA. 062956; Q9Z2N7; Lab DEC-1998 (Rel. 37, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112) ERBB4 OR TYRO-2.
 TIŠSUE=Heart;
MEDLINE=98221155; PubMed=9553078;
Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han X.,
 GVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGC
 -----AENPEYL 1249
 : ||||||||
QEYSTKYFYKQNGRIRPIVAENPEYL 1285
 Rattus norvegicus (Rat)
 1238 KGTPT-----
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 949
 1010
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SEQUENCE OF 1031-1198 FROM N.A.

STRAIN=Sprague-Dawley; TISSUE=Spinal cord;

MEDLINE=97184212; PubMed=9030624;

AMEDLINE=97184212; PubMed=9030624;

AMEDLINE=97184212; PubMed=9030624;

AMEDLINE=97184212; PubMed=9030624;

AMEDLINE=97184212; PubMed=9030624;

AMEDLINE=97184212; PubMed=9030624;

TEXPERSION OF THE PROPERTION.";

-: FUNCTION: SPECIFICALLE BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK: INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.

NOT ACTIVATED BY EGF, AND AMPHIREGULIN (BY SIMILARITY).

-: CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein NOT ACTIVATED BY GF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY).

-: CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein CONT ACTIVATED BY GF, TGF-A, AND AMPHIRESESED IN THE BENELICILAR LOCATION: Type I membrane protein.

-: SUBGELLULAR LOCATION: Type I membrane protein.

-: SUBCELLULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND LULD BERNEY. LOW LEVELS IN KIDNEY, AND LULD LEARN.
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 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4. EXTRACELLULAR (POTENTIAL).
 R INSEPTO; JERO00494; EGFR L domain.

R INTERPRO; JERO00719; Euk pkinase.

R INTERPRO; JERO00719; Euk pkinase.

R INTERPRO; JERO01214; Furin-like.

R INTERPRO; JERO01214; Furin-like.

R INTERPRO; JERO01219; Tyr_pkinase.

R Pfam; PF00137; Furin-like; 1.

R Pfam; PF00137; Furin-like; 1.

R Pfam; PF00130; Recep L domain; 2.

R Pfam; PF00109; TYRKINASE.

R PRODO; PR00109; TYRKINASE.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN MILESETYR; 1.

R TYANGAMENDAMENTIN MILESETYR; 1.

R TYANGAMENDAMENTIN MILESETYR; 1.

R TYANGAMENTIN MILESETYR; 1.

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R TYANGAMENDAMENTIN MILESETYR; 1.

R TYANGAMENDAMENTIN MILESETYR; 1.
 Lai C., Lemke G.;
"An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
 Transferase, Tyrosine-protein kinase, ATP-binding, Phosphorylation. SIGNAL 1 25 POTENTIAL.
 "Neuregulins promote survival and growth of cardiac myocytes. Persistence of ErbB2 and ErbB4 expression in neonatal and adult ventricular myocytes.";
J. Biol. Chem. 273:10261-10269(1998).
 PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY). SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CYTOPLASMIC (POTENTIAL)
 EMBL; AF041838; AAD08899.1; -.
EMBL; U52531; AAC53051.1; -.
HSSP; P11362; 1FGK.
 POTENTIAL.
 POTENTIAL
 TISSUE-Sciatic nerve;
MEDLINE-91222560; PubMed=2025425;
 SEQUENCE OF 848-901 FROM N.A.
M.A., Kelly R.A.;
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 DOMAIN
TRANSMEM
DOMAIN
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| 0                                                   | QY         1003 TFYRSLLEDDDMGDLVDAEEXLVPQQGFFCPDP                                                                  |
|-----------------------------------------------------|--------------------------------------------------------------------------------------------------------------------|
| 334   CYS-RICH.   G   G   G   G   G   G   G   G   G | SEQUENCE  Ouery Match Best Local Sim Matches 612;  I ME 1 ME 1 ME 1 ME 1 ME 1 ME 28 GN 121 LN 122 PS 237 HE 231 HR |

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 Figur, PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00109; Recep_L domain; 2.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SWART; SM00220; S_TKC; 1.
SWART; SM00229; TYKC; 1.
SWART; SM00219; TYKC; 1.
SWART; SM00219; TYKC; 1.
SWART; PF001109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
TYPOSINE; PS50011 kinase; ATP-binding; Phosphorylation; Proto-oncogene.
 KINASE ACTIVITY
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112).
XMRK OR TU.
 Xiphophorus maculatus (Southern platyfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neoperygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyptinodontiformes; Poecillidae; Xiphophorus.
 [1] = SQUENCE FROM N.A. MEGGE 2797166; Maneler W., Raulf F., MEDLINE 90015140; PubMed = 2797166; Mittbrodt J., Adam D., Mailtschek B., Maueler W., Raulf F., Telling A., Robertson S.M., Schartl M.; Thoyel putative receptor tyrosine kinase encoded by the melanomaninducing Tu loous in Xiphophorus."; Nature 341:415-421(1989).
 Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACT:
-:- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 MELANOMA RECEPTOR PROTEIN-TYROSINE
 tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNAT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 KINASE.
EXTRACELLULAR (POTENTIAL)
 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PROTEIN KINAGE.
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 HSSP, P11362; IFGK.
InterPro; IRR000494; EGFR L domain.
InterPro; IRR00719; EUk pkinase.
InterPro; IRR002194; Furin-like.
InterPro; IRR002290; Ser_thr_pkinase.
InterPro; IRR001245; Tyr_pkinase.
 EMBL; X16891; CAA34770.2; -.
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 PIR; S06142; S06142.
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REVISION TO 515.
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| 245 BY SIMILARITY. 253 BY SIMILARITY. 265 BY SIMILARITY. 266 BY SIMILARITY. 210 BY SIMILARITY. 310 BY SIMILARITY. 311 BY SIMILARITY. 312 BY SIMILARITY. 313 BY SIMILARITY. 314 BY SIMILARITY. 315 BY SIMILARITY. 317 BY SIMILARITY. 318 BY SIMILARITY. 319 BY SIMILARITY. 310 BY SIMILARITY. 311 BY SIMILARITY. 312 BY SIMILARITY. 312 BY SIMILARITY. 313 BY SIMILARITY. 314 BY SIMILARITY. 315 BY SIMILARITY. 316 BY SIMILARITY. 317 BY SIMILARITY. 318 BY SIMILARITY. 319 BY SIMILARITY. 320 BY SIMILARITY. 331 BY SIMILARITY. 332 BY SIMILARITY. 333 BY SIMILARITY. 344 BY SIMILARITY. 355 BY SIMILARITY. 356 BY SIMILARITY. 357 BY SIMILARITY. 358 BY SIMILARITY. 359 BY SIMILARITY. 350 BY SIMILARITY. 350 BY SIMILARITY. 350 BY SIMILARITY. 351 BY SIMILARITY. 352 BY SIMILARITY. 353 BY SIMILARITY. 354 BY SIMILARITY. 355 BY SIMILARITY. 356 BY SIMILARITY. 357 BY SIMILARITY. 358 BY SIMILARITY. 359 BY SIMILARITY. 350 BY SIMILARITY. 360 BY SIMILA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 39.9%; Score 2715.5; DB 1; Length 1167;<br>ty 45.4%; Pred. No. 1.7e-138;<br>ervative 162; Mismatches 387; Indels 145; Gaps | AALCRWGLLLALLPPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCOVVQGN 5<br>    : | FLQDIQEVQGYVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN<br> | YIKANSKFIGITELOLRSLTEILKGGVLIORNPOLCYODTILWKDIFHK | NNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTD 2 | CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS | CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR 3 | EFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISA<br> : | WPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTH 4 | LCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQ 5 | FLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDP 5 | PFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS 6 |
| 23.7<br>26.9<br>30.0<br>30.0<br>30.0<br>30.0<br>50.0<br>50.0<br>50.0<br>50.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | similarity<br>77; Conser                                                                                                   | AALCRWG                                                             | LELTYLPTNASLS   :        LEITYTQENQDLS              | GDPLNNQ                                           | NNQLALT<br>: :<br>TSNPTMN                                      | CCHEQCAAG<br>  :      <br>CCNEHCAGG                 | CVTACPY<br>     <br>CVKECPS                                    | AVTSANIQ<br>       :<br>AVNSTNIR                           | WPDSLPD<br>  :::<br>WPENMTS                                    | LCFVHTV<br>  :: :<br>LRYANTI                                   | FLRGQEC<br>    <br>VDRGGRC                                     | PFCVARC                                                        |
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| F114<br>F114<br>F114<br>F114<br>F114<br>F114<br>F114<br>F114                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ŌĂĬ                                                                                                                        | ò q                                                                 | o da                                                | 90 ر                                              | λ <sub>0</sub> α                                               | oy<br>DP                                            | ර් සි                                                          | ò a                                                        | පි පි                                                          | දි සි                                                          | රු සි                                                          | ò                                                              |

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954 IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD 1013
 1014 MGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRS 1073
 1074 PLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVAPLT 1132
 CSPOPEYVNOPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSPGKNG 1179
 1057 ----EYVNOPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNTNQNS 1111
 703
 763
 833
 823
 893
 883
 894 ILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM 953
SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALES
 654 IVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMR
 ILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAVV
 1022 PCIPPTGH------PVRENSITLRNISDPTQNALEKDLDGH----
 1180 VVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKG
 MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbb-3 precursor (EC 2.7.1.112)
(C-erbB) (Tyrosine kinase-type cell surface receptor HER3).
ERBB3 OR HER3.
 Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A., "Isolation and characterization of ERBB3, a third member of the ERBB/epidermal growth factor receptor family: evidence for overexpression in a subset of human mammary tumors."; Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
 PRT; 1342 AA.
 MEDLINE=90083234; PubMed=2687875;
 SEQUENCE FROM N.A.
MEDLINE=30311312; PubMed=2164210;
 1240 TPTAENPEYLG 1250
 1147 LPAAENLEYLG 1157
 STANDARD;
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 ERB3 HUMAN
P21860;
 1112
 884
 1001
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 (POTENTIAL).

- I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND SECRETED (SHORT FORM).

- I- ALTERNATIVE PRODICTS: TWO PORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

- I- TISSUE SPECIFICITY: EPTTHELLAL TISSUES AND BRAIN.
- I- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
- PTW: LIGAND-BINDING INVERASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIPYLINGSITOL 3-KINASE (BY SIMILARITY).
- IL SIBLEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.
- I- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
lowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L.,
 Pfam; PF00069; DKINIASE, 1
Pfam; PF00069; DKINIASE, 1
Pfam; PF00157; Furin-like; 1
ProDom; PD000001; Euk Dkinase; 1.
SMART; SM00261; FU; 3
SWART; SM00219; TYKC; 1
SWART; SM00219; TYKC; 1
PROSITE; PS00109; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE TYR; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE TYR; FALSE NEG.
Transmembrane; Glycoprocefin; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 Todaro G.J., Shoyab M.;
"Molecular cloning and expression of an additional epidermal growth
Eactor receptor-related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990).
 tyrosine Kinase.";
Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEURECULINS AND NTAK.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 TISSUE=Placenta;
MEDLINE=91282825. PubMed=7685162;
KATOh M., Yazaki Y., Sugimura T., Terada M.;
"C-erbB3 gene encodes secreted as well as transmembrane receptor
 Cyrosine phosphate.
 CYTOPLASMIC (POTENTIAL)
 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 SIMILARITY.
SIMILARITY.
SIMILARITY.
 InterPro; IPR000494; EGFR L domain
InterPro; IPR000719; Buk pkInase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
 SEQUENCE FROM N.A. (SHORT FORM).
 EMBL; M29366; AAA35790.1; -...
EMBL; M34309; AAA35979.1; -...
EMBL; G51953; AAB26935.1; -...
PTR; A36223; A36223.
HSSP; P11362; IFGK.
 643
664
1342
966
723
742
834
194
 (POTENTIAL)
 MIM; 190151; -
 ACT SITE
DISULFID
DISULFID
 NP BIND
BINDING
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999

604 593 719

651

779 768 839

708

899 888 959 948

828

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MIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPA---SPLDSTFYRSLLEDDDMGD 1016
 474 LRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHC
 KPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA----SPLTSIVSAVVG
 TGSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVM
 FRNPHQALLHTA - NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEEC
 661 ILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETE
 PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDV
 1017 LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEP-SEEEAPRSPL
 1076 APSEGAGSDVFDGDLGMGAAKGLQSLPTHD-PSPLQRYSEDPTVPLP----SETDGYV
 :|| | : |:|| : |:|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |
 A------
 PDTHLKGTPSSREGTLSSVGLSSVLGTEEEDED-----EEYEYMNRRRHSP-PHPP
 PAARPAGATLERAKTLSP-GKNGVV-----KDVFAFGGAVENPEYLTPQGGAAPQPHPP
 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
 1211 PAFSPAFDNLYYWD-------QDPPERGAPPSTFKGTPTAENPEYL 1249
 RPSSLEELGYEYMDVGSDLSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYM 1263
 ERB3 RAT STANDARD; PRT; 1339 AA.
062799; Q62955;
15-DG-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2003 (Rel. 41, Last annotation update)
16-JUN-2003 (Rel. 41, Last annotation update)
17-JUN-2003 (Rel. 41, Last annotation update)
18-JUN-2003 (Rel. 41, Last annotation update)
18-JUN-2003 (Rel. 41, Last annotation update)
 [1]
SEQUENCE FROM N.A.
 720
 840
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 N-LINKED (GLCNAC. .) (POTENTIAL).
ELIGGGVIERODECHMOLED TOWNORR
SC -> GOFPWYSGLTPQPAQDWYLLDDDPRLLTLSASSK
VPVTLAAV (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
E -> G (IN REF. 2).
E -> G (IN REF. 2).
E -> G (IN REF. 2).
 127
 187
 178
 246
 237
 306
 353
 426
 413
 485
 473
 70
 |||| :|
|GLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGH
 128 IKANSKFIGITELQLRSLTEILKGGVLJQRNPQLCYQDTILWKDIFHKNNQLALTLIDTN
 DVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAG
 PKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST
 NLOVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQL
 GLLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT
 NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNQY
 RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG
 CKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQ
 Gaps
 (POTENTIAL).
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(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 Ouery Match 35.7%; Score 2430.5; DB 1; Length 1342; Best Local Similarity 40.5%; Pred. No. 4e-123; Matches 531; Conservative 192; Mismatches 459; Indels 129;
BY SIMILARITY.
BY SIM
 148097
 1342
560
1064
 184 1342
560 560
1064 1064
1342 AA; 1
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 SUBCELLULAR LOCATION: Type I membrane protein.

DOWAIN: THE CYTOPLASNIC PART OF THE RECEPTOR MAY INTERACT WITH THE BOAD OR SH3 DOWAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE PBS SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
EXTRACELLULAR (POTENTIAL).
 STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
MEDLINE=97184212; PubMed=9030654;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
Expression of neurogulins and their putative receptors, ErbB2 and
ErbB3, is induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997).
J. Neurosci. 17:1642-1659(1997).
J. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=96096535; PubMed=8522190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.;
"Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.";
Gene 165:279-284(1995).
 tyrosine phosphate.
 REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 CYTOPLASMIC (POTENTIAL) CYS-RICH.
 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
 lJJ
SEQUENCE OF 922-1097 FROM N.A.
CTDAIN=SOTAGUE-DAWley; TISSUE=SCÍALIC NELVE;
 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 EMBL, US2530; AACS0050.1; -.
HSSP; P11362, 1FGK.
INTERPRO, IPR00049; EGFR L domain.
INTERPRO, IPR000719; EUK DKIABSE.
INTERPRO, IPR002174; FUXIN-like.
INTERPRO, IPR002174; FUXIN-like.
 EMBL; U29339; AAC28498.2; -.
 643
662
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Query Masst Loc<br>Matches                                                                                                | රු සි                                                          | & 8                                                                     | <b>상</b> 옵                                                           | රු සි                                                                   | & 8                                                                    | ò a                                                                  | ò 8                                                                    | \<br>6                                                             | & 43                                                                 | දු දු                                                                | ò                                                               |
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Clifford R., Schupbach T.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

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IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD 1013
 1014 MGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE---- 1068
 1024 LGSALSLPTGTLTRPRGSQSLLSPSSGYMPMNQSSLGEACLDSAVLGGREQFSRPISLH- 1082
 1146 RPOPPSPREGP-----KDVFAF 1187
 | :| | : | : | : | : | ILTPVTPLSPPGLEEEDGNGYVMPDTHLRGASSSREGTLSSVGLSSVLGTEEEDED---- 1191
 643
 773
 833
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 953
 D EGFR_DROME STANDARD; PRT; 1426 AA.

C P04412; OG1601; O9W2G0; P81868;
T 13-AUG-1987 (Rel. 05, Created)
T 15-DEC-1998 (Rel. 37, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
E Pidermal growth factor receptor precursor (EC 2.7.1.112) (Egfr)
E Gurken receptor) (Torpedo protein) (Drosophila relative of ERBB).
B GGR OR C-ERBB OR DR OR GG10079.
C Edvaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
C Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
C Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
894 ILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM
 : :: ||||:| |::||||| :| ||||| || |||| ||| |||| ||| ||| ||| ||| ||| ||| VGSLDHAHIVRLIGLGLCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLNMGVQIAKGM
 SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALES
 655 VSAVVGILLVVVLGVVFGILIKRRQOKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMR
 ILKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYV
 774 MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM
 -----EAPRSPLAPSEG-----AGSDVFDGDLGMGAAKGLQSLPTHD
 PIPRGR -----PASESSEGHVTGSEAELQEKVSVCRSRSRSRSPRPRGDSAYHSQRHS
 PSPLORYSEDPTVPLPSETDGYV----APL----TC-----SPQPE----YVNQPDV
 SEQUENCE FROM N.A. (ISOFORMS TYPES I AND II).
MIDLINE-34352020; PubMed-8070664;
Clifford R., Schupbach T.;
"Molecular analysis of the Drosophila EGF receptor homolog reveals that several genetically defined classes of alleles cluster in subdomains of the receptor protein.";
Genetics 137:531-550(1994).
 GGAVENPEYLTPQGGAAPQPHPP 1210
 ----EEYEYMNRKRRGSP-PRPP 1209
 [2]
REVISIONS.
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TRAINEBERKEING, NEW A. A. SCHOLE R. A., EVANS C. A., GOCGAME J. D., RA Amanatides P. G., Scherer S. E. Li P. W., Hookins R. A., Galle R. F., GOCGG R. A., Howler S. E., Holt R. A., Evans C. A., Gocgyne J. D., Adams M. D., Celniker S. E. Li P. W., Hookins R. A., Galle R. F., Gocgge R. A., Howler S. E., Holt R. A., Shabumer M., Henderson S. N., Butcher G., Mortman J. R., Yandell M. D., Zanng G., Chen L. X., Brandon R. C., Rogers Y. H. C., Blazel R. G., Champe M., Pfeiffers B. D., Randon R. C., Rogers Y. H. C., Blazel R. G., Champe M., Pfeiffers B. D., Bardon R. C., Bardon R. R., Benos P. V., Berman B. P., Bhandari D., Bolshakov S., Butris R. Y., Benos P. V., Berman B. P., Bhandari D., Bolshakov S., Burkis R., Benos P. V., Berman B. P., Bhandari D., Bolshakov S., Burkis R., Bassley E. M., Cawley S., Daller R., Carris G., Carlon H. R., Bouck J., Brokstein P., Brottier P., Brottier P., Bortler A., Candre R. A. Belos B., Delcher A., Deng Z., Mays A.D., Dew I., Diet Z. S. M. A. Candre R. Delcher A., Deng Z., Mays A.D., Dew II., Diet Z. S. M. A. Delcher A., Deng Z., Gann R. D., Dew II., Diet Z. S. M. A. Dedon K. J., Brownes M., Dugann-Rochas S., Dunkov B. C., Dunn P., Bottin R. J., Elbownes M., Dugann-Rochas S., Dunkov B. C., Dunn P., Durbin K. J., Evangelisae C. C., Ferriaz C., Glabrita M. E., Gorrell J. H., Gu Z., Gann P., Harris M., Harrey D., Henman T. J., Hernandez J. R., Houck J., Bartey D., Henman T. C., Mennison J. A., Rochman E., Kodita C. D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang V. Matteri B., McInches T. C., Morris J., Moscher D. D., A. Hould M. J., McLod M. S., Mount S. M., Mount S. M., Mount S. M., Moy M., Mutphy B., Mutphy L., Mutzny D.M., Nelson D.L., Rhe Reinert K., Remington K., Sunders R., Wender B., Spier E., Spradling A.C., Staalecon M., Stups R., Melson D.K., Stale B., McInchos J., Singen M., Mutphy B., Mutphy M., Mutphy B., Mutphy M., Mutphy M., Mutphy B., Mutphy M., Mutp
 SEQUENCE FROM N.A. (ISOFORM TYPE I), TISSUE SPECIFICITY, AND MUTATION
 Lesokhin A.M., Yu S.-Y., Katz J., Baker N.E.;
"Several levels of EGF receptor signaling during photoreceptor specification in wild-type, Ellipse, and null mutant Drosophila.";
Dev. Biol. 205:129-144(1999).
 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=85124611; PubMed=2982499;
Livneh E., Glazer L., Segal D., Schlessinger J., Shilo B.-Z.;
"The Drosophila EGF receptor gene homolog: conservation of both hormone binding and kinase domains.";
Cell 40:599-607(1985).
 MEDLINE-85137938; PúbMed-2983232;
Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
"A Drosophila genomic sequence with homology to human epidermal
 SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE SPLICING
STRAIN-Oregon-R; TISSUE=Embryo;
MEDLINE=87002474; PubMed=3093080;
 οţ
 Schejter E.D., Segal D., Glazer L., Shilo B.-Z.;
"Alternative 5' exons and tissue-specific expression
Drosophila EGF receptor homolog transcripts.";
Cell 46:1091-1101(1986).
 SEQUENCE FROM N.A. (ISOFORM TYPE I).
 MEDLINE=99102120; PubMed=9882502;
 SEQUENCE OF 959-1078 FROM N.A.
 STRAIN=Daekwanryeong;
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CELL 89:13-16(1997).

CELL 89:13-16(1997).

CELL REFERENCE THE STATE, GURKEN, VEIN AND ARGOS,
CC WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-
CC MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.
CC CRITICAL FOR THE PROLIERRATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTBRIOR AND DORSO-VENTRAL CC ESTABLISHMENT OF VENTRAL CELL FATES, MAINTERNACE OF AMIOSEROSA AND VENTRAL NEUROBECTODERMAL CELLS, GERM BAND RETACTION, CELL FATE CS PROLICION.

CC SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
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 TYPE III, ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SERN IN WING DISKS, GENITAL DISK, HIGHEST
EXPRESSION IS AND BALIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
 ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND
 Perrimon N., Perkins L.A.; "There must be 50 ways to rule the signal: the case of the Drosophila
 Raz E., Schejter E.D., Shilo B.Z.,
"Interallelic complementation among DER/flb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
 tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
 EMBL, AF052754; AAC08536.1; --
EMBL, AF052754; AAC08536.1; --
EMBL, AF052754; AAC08536.1; JOINED.
EMBL, AF0527754; AAC08535.1; --
EMBL, K03471; AAA51462.1; --
EMBL, K03418; AAA51462.1; --
EMBL, K03418; AAA51461.1; --
EMBL, AF109079; AAD26134.1; --
EMBL, AF109079; AAD26132.1; JOINED.
EMBL, AF109081; AAD26133.1; --
EMBL, AF109079; AAD26133.1; JOINED.
EMBL, AF109079; AAD26130.1; JOINED.
EMBL, AF109079; AAD26130.1; JOINED.
 MEDLINE=92038942; PubMed=1936959;
 MEDLINE=97248481; PubMed=9094709;
 CAA26157.1; -.
 CAA55523.1; -.
 growth factor receptor.";
 Nature 314:178-180(1985)
 X78918;
 PROTEIN
 ANALYSIS
 REVIEW
 EMBL;
 EMBL;
EMBL;
 EMBL;
EMBL;
 EMBL;
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42
 159
 137
 203
 197
 255
 375
 428
 488
 486
 204 YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE 263
 264 SCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDCIAC 322
 256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 315
 381
 427
 82
 549 KEPBÓKVWVNENLRAĎLCEKNGTICSDOCNEDGCWGAGTDÓCLTCKNFNFNGTCIADCGY 608
 LQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP---- 601
 PQDKMDKGGE-----CVPCNGPCPKTCPGVTVLH-----AGNIDSFRNCTVIDGNIR
 TELOLRSLTEILKGGVLIORNPOLCYODTILWKDIFHKNNQLALTLIDTNRSRACHPCSP
 198 MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA
 376 FLPESFDG--DPASNTA-----PLOPEQLOVFETLEEITGYLYISAWPDSLPDLSVFQN
 429 ILDQTFSGFQDVYANYTMGPRYIPLDPERREVFSTVKEITGYLNIEGTHPQFRNLSYFRN
 LOVIRGRILHNGAY-SLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLF
 RNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRV
 QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT-NASLSFLQDIQEVQG
 83 YVLIAHNQVRQVPLQRLRIVRGTQLF-----EDNYALAVLDNGDPLNNQYIKANSKFIGI
 323 KNFFDEAVSKEECPPMRKÝNPTTYVLETNPEGKYAYGATCVKECP-GHLLRDNGACVRSC
 BY SIMILARITY.
PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
 Gaps
 Transmembrane; GlycoproteIn; Receptor; Phosphorylation; Transferase; Tyrosine-protein kinase; ATP-binding; Signal; Alternative splicing;
 Conservative 184; Mismatches 431; Indels 338;
 EPIDERMAL GROWTH FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
 Length 1426;
 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PROPEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
 Score 1976; DB 1;
Pred. No. 1.1e-98;
 ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 7.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00109; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 POTENTIAL.
 InterPro; IPR000494; EGFR L. domain.
InterPro; IPR000119; Euk pkinase.
InterPro; IPR001145; Furin-like.
InterPro; IPR001145; Tyr pkinase.
Pfam; PF001059; pkinase; 1.
Pfam; PF001030; Recep L. domain; 2.
PKINTS; PR00109; TYRKINASE.
PY0000m; PD000001; Euk pkinase; 1.
 29.0%;
EMBL, X78919; CAA55522.1; -
PIR; A00640; GQFFE.
HSSP; P11362; 1FGK.
FlyBase; FBgn0003731; Egfr.
 Developmental protein.
 Similarity
 471;
 TRANSMEM
DOMAIN
DOMAIN
 ACT_SITE
MOD_RES
 316
 487
 382
 428
 Query Match
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 1196 EFARDPGRYLAIPGDKFTRLPA------YTSQDEKDLIRKLAPTTDGSEAIAKPDDYLQ 1248
 777
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 619
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 737
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 857
 917
 IWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLV 797
QKIRKYT - - MRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKG
 PDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP-----RSPLAPSEGAGSDVP
 DVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL----TP
 DRGVCRECHATCDGCTGPKDTIGIGACTTCNLAIINNDATVKRCLLKDDKCPD-GY--FW
 EYVHPQEQGSLKPLAGRAVCRKCHPLCELCTNYGYHEQVCSKCTHYKRREQCETECPADH
 YTDEEQRECFORHPECNGCTGPGADDCKSCRNFKLFDANETGPYVNSTMFNCTSKCPLEM
 ----IVSAVVGILLVVVLGVVFGILIKRRO
 TQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPN
 HVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMT
 FGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFS
 DG---DLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQP
 ----PDLSYMPIW
 RMARDPORFVVIQNEDLG--PASPLDSTFYRSLLEDD----DMGDLVDAEEYLVPQQGFFC
 -----DEMPKLNRYCKDPSNKNSSTGDDER
 2.7.1.112).
 1200 QGGAAPQPH-------PPPAFSP-AFDNLYYWD 1224
 1365 GVGESPIPTOTIGIPVMGGPGTMEVKVPMPGSEPTSSDHEYYND 1408
 ---SC----VDLDDKG----
 Viruses; Retroid viruses; Retroviridae; Alpharetrovirus NCBI TaxID=11864; [1]
 21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC
 634 AA
 KF--PDEEGACQP-------CPI---
 ---ASPLTS---
PKAAPGPS-----HRTDCT
 STANDARD;
 Avian leukosis virus.
 926
 1016
 828
 1076
 1136
 1144
 ERBB ALV
P00534;
 609
 178
 738
 1033
 1249
 1288
 1326
 718
 647
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 V-ERBB.
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 17;
 646
 705
 117
 765
 177
 825
 237
 882
 297
 28
 587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
 706 MPNOAOMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
 EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
 tyrosine phosphate.
-!- MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS
IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS
AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY
THE INSERTION OF RETROVIAGAL PROMOTER ELEMENTS IN OR NEAR THE
C-ERB GENE, WHICH LEADS TO C-ERBB ACTIVATION.
-!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
 Gaps
 -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 123;
 Length 634;
 Oncogene;
 novelion of
 Indels
 Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M., Crittenden L.B., Raines M.A., Kung H.-J.;
"c-erbB activation in ALV-induced erythroblastosis: nov processing and promoter insertion result in expression amino-truncated EGF receptor.";
Cell 41:719-726 (1985).
 70891 MW; E705E33A0BE01FCC CRC64;
 PIR, MO0643; TVCHLV.

RISSP, P11362; ITVCHLV.

INTERPO; IPR000719; Euk_pkinase.

InterPro; IPR0001245; Tyr_pkinase.

REINTS, PR00109; TYRKINASE.

RPRINTS, PR00109; TYRKINASE.

RPROSCHE; PS00107; PROTEIN KINASE ATP; 1.

RPROSITE; PS00109; PROTEIN KINASE DOM; 1.

RPROSITE; PS50011; PROTEIN KINASE DOM; 1.

RPROSITE; PS50011; PROTEIN KINASE DOM; 1.

REAST; PROSITE; PS50011; PROTEIN KINASE DOM; 1.

REAST; PROSITE; PS50011; PROTEIN KINASE DOM; 1.

REAST; PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 DB 1;
 25.7%; Score 1749.5; DB 1; 52.3%; Pred. No. 6e-87; ive 79; Mismatches 135;
 PROTEIN KINASE.
ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
 BY SIMILARITY
 EMBL; M10066; AAA48763.1; ALT_INIT
LINE=85228222; PubMed=2988784;
 Phosphorylation.
 Best Local Similarity 52.3
Matches 370; Conservative
 165
 146
 257 ;
634 AA;
 Glycoprotein;
DOMAIN
 NP BIND
BINDING
ACT SITE
SEQUENCE
 647
 59
 994
 178
 826
 238
 Query Match
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IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP

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 ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF 1004
 1177
 YRSILEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1064
 1178 NGVVKDVF------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY 1222
 SEUENCE OF 1-152 FROM N.A.

MEDLINE-84223957; PubMed=6528658;

MEDLINE-8423957; PubMed=6528658;

MEDLINE-8423957; PubMed=6528658;

Saule S., Martin P., Stehelin D.;

"Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of oncogene.";

"Graucing the erbA gene of avian erythroblastosis virus reveals a ceince 224:1456-1456(1984).

-! GYALVITC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-! DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND EXTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROBLASTS.
K.;
 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP
 1120 LPSET - DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK
 -----TAMVQ
 MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE RECEPTOR FOR EPIDERMAL GROWTH FACTOR. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima "The erbB gene of avian erythroblastosis virus is a member of the
 Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 (EC 2.7.1.112)
 1223 WDQ-----DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1254
 FLEESIDDGFL-----PAPEYVNQ--LMPKKPS-----
 21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB
 604 AA
 PRT;
 MEDLINE=84026539; PubMed=6313229;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
15-JUN-2002 (Rel. 41, Last ann
 STANDARD;
 35:71-78(1983).
 FROM N.A.
 IN CHICKENS
 ERBB AVIER
ID ERBB AVIER
AC P00535;
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16;
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 946 ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF 1004
 417
 1005 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1064
 1065 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
 1120 LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1177
 ---GGAVENPEYLTPQGGAAPQPHPPPAFSPAFD 1218
 117
 765
 825
 885
 945
 449
 177
 297
 298 IKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPP 357
 58
 647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
 59 NGSKTPSIAAGUVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
 587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
 3 CAHFIDGPHCVKACPAGVLGENDTL-VRKYADANAVCQLCHPNCTRGCKGPGLEGCP---
 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANK
 BILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
 CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
 -----RNGOGHPVREDSFVQRYSSDPTGN
 ---NTNOSPLAKTVFE
 Gaps
 76; Mismatches 128; Indels 126;
 Length 604;
 76EBCDD06745D609 CRC64;
 525 ---VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL----
 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
R -> W (IN REF. 2).
S -> F (IN REF. 2).
I -> V (IN REF. 2).
 DB 1;
 Pred. No. 1.8e-84
 1219 NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1248
 25.0%; Score 1703; 52.2%; Pred. No. 1.6
 K02006; AAA42394.1; ALT_INIT
K01216; AAA42400.1; -.
 Phosphorylation
 67633 MW;
 Best Local Similarity 52.29
Matches 360; Conservative
 165
257
29
140
 1178 NGVVKDVFAF--
 140
146
104 AA;
 Glycoprotein;
DOMAIN 13
 NP_BIND
BINDING
ACT_SITE
CONFLICT
CONFLICT
 358
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EILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNIGSQYLLNW 237
 01.JAN-1990 (Rel. 13, Created)
01.JAN-1990 (Rel. 13, Last sequence update)
01.JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC
 703 AA
 PRT;
 1179 GVVKDVFAFGGAVENPEYL 1197
 MEDLINE=88261272; PubMed=3260329;
 : ||:|||||
|-----SHSTAVDNPEYL
 STANDARD;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9031;
 EGFR CHICK
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 14;
 705
 117
 765
 825
 58
 SEQUENCE FROM N.A.
MEDLINE=87064458; PubMed=2878364;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbB confers a thermolabile phenotype to ts167 avian erythroblastosis virus-transformed erythroid
 EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNM
 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
 CAHYKOPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
 Gaps
 Viruses, Retroid viruses, Retroviridae, Avian type C retroviruses.
VCBI_TaxID=103898,
 (EC 2.7.1.112)
 MOI. Cell. Biol. 6:1751-1759(1986).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 90;
 HSSP, P11362; 1FGK.
InterPro; 1PR001245; Tyr_pkinase.
InterPro; 1PR001245; Tyr_pkinase.
Pfam; PF00069; ppinase; 1.
ProDom; P0000001; Euk_pkinase; 1.
SMART; SM01219; TyrKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyresine-protein kinase; ATP-binding; Oncogene;
 Length 540;
 -> D (IN THERMOLABILE V-ERBB)
 69; Mismatches 119; Indels
 5B53297AA068B65D CRC64;
 -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 Tyrosine-protein kinase transforming protein erbB V-ERBB.
 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
 23.9%; Score 1630; DB 1; 55.1%; Pred. No. 1.3e-80;
 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
 Avian erythroblastosis virus (strain ts167).
 594
 PROTEIN KINASE
 BY SIMILARITY
----INLDNPDY
 60412 MW;
 horylation
 EMBL; M13179; AAA42401.1; -. PIR; A25231; TVFVEB.
 SSPYWIQSGNHQ----
 Conservative
 STANDARD;
 tyrosine phosphate
 Phosp
 540 AA;
 Similarity
 Glycoprotein;
 ERBB AVIEU
 341;
575
 587
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946 ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLGPASPLDSTF 1004
 1005 YRSILEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1064
 1065 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
 1120 LPSETDGYVAPLTCSPQPEYVNOPDVRPQPPSPREGPLPAARPAGAT-LERAKTLSPGKN 1178
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 417
 945
 298 IKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPP 357
 885
 297
 449
 527
 AND
CMOIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
 238 CVQIAKGMNYLEERHMVHRDLAARNVLVKTPQHVKITDFGLAKQLGADEKEYHAEGGKVP
 886 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 cell DNA
 -PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLTAISKLPIDSRYQN
 Lax I., Johnson A., Howk R., Sap J., Bellot F., Winkler M.,
Ullrich A., Vennstrom B., Schlessinger J., Givol D.,
Chicken epidermal growth factor (EGF) receptor: cDNA cloning,
expression in mouse cells, and differential binding of EGF and
transforming growth factor alpha.,
Mol. Cell. Biol. 8:1970-1978(1988)
--- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AN
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY)
--- CAPALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 2.7.1.112) (CER)
 418 YRTLMEEEDMEDIVDADEYLVPHQGFF------NSPST----
 tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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11;
 121
 181
 61
 72
 RWGLLLALLPPGAA----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
 LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD
 122 PLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL
 TLID-INRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGGA-RCKGPLPTDCCHEO
 Ouery Match 23.7%; Score 1614; DB 1; Length 703;
Best Local Similarity 44.3%; Pred. No. 1.3e-79;
Matches 313; Conservative 113; Mismatches 253; Indels 28; Gaps
 (POTENTIAL).
(POTENTIAL).
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 EMBL; M20386; AAA40760.1; -.
R InterPro; IPR00019; Euk, pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Pfam; PF00107; Furin-like; 1.
R Pfam; PF010757; Furin-like; 1.
R PR0SITE; PS00107; PROTEIN KINASE ATP; PARTIAL.
R PROSITE; PS00107; PROTEIN KINASE TYR; PARTIAL.
R PROSITE; PS00107; PROTEIN KINASE TYR; PARTIAL.
R PROSITE; PS00107; PROTEIN KINASE DOM; PARTIAL.
R PROSITE; PS001107; PROTEIN KINASE DOM; PARTIAL.
R PROSITE; PS001107; PROTEIN KINASE DOM; PARTIAL.
R PROSITE; PS00117; PROTEIN KINASE DOM; PARTIAL.
R TYROSINE; PS00117; PROTEIN KINASE DOM; PARTIAL.
R TYROSINE DOLO; PROTEIN KINASE DOM; PARTIAL.
TYROSINE PROSITE; PS00117; PROTEIN KINASE DOM; PARTIAL.
TYROSINE PROTEIN KINASE; ATP-binding; Phosphorylation.
SIGNAL 1 30
EPIDERWAL GROWTH FACTOR RECEPTOR.
 EPIDERMAL GROWTH FACTOR RECEPTOR
 EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYOPOLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARIT
 77427 MW; AFF2DE11B735A690 CRC64;
 (GLCNAC. . .)
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 NIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL
 ||::| :|| || ||: || || CVKQCNILQGEPREFERDSKCLPCHSECLVQNSTAYNTTCSGPGPDHCMKCAHFIDGPHC
TVLDFASNLSSCPKCHPNCTEDHCWGAGEQNCQTLTKVICAQQCSGRCRGKVPSDCCHNQ
 CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
 243 CAAGCTGPRESDCLACRKFRDDATCKDTCPPLVLYNPTTYQMDVNPEGKYSFGATCVREC
 PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSA
 VPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQE
 CVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAHYKDPPFC
 597 VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS
 PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
 703
 657 AVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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July 22, 2003, 08:22:34; Search time 48.3575 Seconds (without alignments) 5347.444 Million cell updates/sec Run on:

SEQ4-103-117-12
6809
1 MELAALCRWGLLIALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255

Title: Perfect score: Sequence:

671580 seqs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched: 671580

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 21:\* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:

| Description                   | O18735 canis famil<br>Q9qx70 rattus norv | O9ep98 mus musculu O9yh40 xiphophorus | P79754 fugu rubrip<br>O9bih9 anopheles o | Q9uk79 homo sapien<br>Q8r2x1 mus musculu | Q86712 avian rous-        |        | Q85468 avian eryth<br>Q9wvf5 mus musculu<br>Q9erv6 mus musculu |
|-------------------------------|------------------------------------------|---------------------------------------|------------------------------------------|------------------------------------------|---------------------------|--------|----------------------------------------------------------------|
| SUMMARIES                     | 018735<br>Q9QX70                         | Q9EF98<br>Q9YH40<br>Q9W6F6            | P79754<br>09BIH9                         | Q9UK79<br>Q8R2X1                         | Q86/12<br>Q86714<br>Q8WVV | Q64895 | Q85468<br>Q9WVF5<br>Q9ERV6                                     |
| DB                            | 111                                      | 13                                    | 13                                       | 411                                      | 15                        | 15     | 111                                                            |
| %<br>Query<br>Match Length DB | 1259                                     | 1165                                  | 1328                                     | 419                                      | 567                       | 962    | 655<br>643                                                     |
| %<br>Query<br>Match           | 91.8                                     | 40.4                                  | 34.0                                     | 26.4                                     | 25.2                      | 24.3   | 22.3                                                           |
| Score                         | 3156                                     | 2729.5                                | 2315                                     | 1798.5                                   | 1718                      | 1653.5 | 1519.5<br>1503.5                                               |
| Result<br>No.                 | 100                                      | ט ישייט                               | 9                                        | <b>ω</b> ο .                             | 11                        | 13.    | 15                                                             |

| O9vlx8 ephydatia f |        | Q26566 schistosoma |        | Q9ese0 rattus norv | Q9psh2 gallus gall | Q14256 homo sapien | Q923v5 rattus norv | P11776 xiphophorus | Q8szwl drosophila | Q9pvz4 xenopus lae | 099162 xiphophorus | O9niv5 biomphalari | O9bud7 homo sapien | O9bq66 oryctolagus | Q8uw85 paralichthy | 093457 scophthalmu |        | O73798 xenopus lae | Q9u5a8 bombyx mori | Q8uw84 paralichthy | O8uw83 paralichthy | O9ygh8 scophthalmu | O9qvw4 rattus sp. | Q9vd94 drosophila | Q91ym0 mus musculu | Q96135 homo sapien |        | Q07912 homo sapien |
|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------|--------------------|
| 09Y1X8             | 023821 | 026566             | 090836 | O9ESEO             | Q9PSH2             | 014256             | Q923V5             | P11776             | QBSZW1            | Q9PVZ4             | 099162             | Q9NJV5             | Q9BUD7             | 09BG66             | Q8UW85             | 093457             | QBUW86 | 073798             | Q9U5A8             | Q8UW84             | Q8UW83             | Q9YGH8             | Q9QVW4            | Q9VD94            | 091YM0             | Q96L35             | Q99MR2 | 007912             |
| ß                  | ß      | ഹ                  | 13     | 11                 | 13                 | 4                  | 11                 | 13                 | 'n                | 13                 | 13                 | s                  | 4                  | φ                  | 13                 | 13                 | 13     | 13                 | Ŋ                  | Ξ                  | 13                 | 13                 | 7                 | S                 | Ξ                  | 4                  | 11     | 4                  |
| 1193               | 1368   | 1717               | 527    | 478                | 599                | 165                | 176                | 346                | 435               | 1362               | 311                | 1671               | 331                | 149                | 1368               | 1418               | 1369   | 1358               | 1472               | 1412               | 1418               | 1245               | 1371              | 2144              | 987                | 935                | 987    | 1036               |
| 18.9               | 17.9   | 17.1               | 16.8   | 14.9               | 14.1               | 13.3               | 13.0               | 11.8               | 11.4              | 11.1               | 11.1               | 10.7               | 10.6               | 10.6               | 10.3               | 10.2               | 10.0   | 6.6                | 9.8                | 9.6                | 9.5                | 9.4                | 9.4               | 9.1               | 8.8                | 8.7                | 8.7    | 9.6                |
| 1288               | 1215.5 | 1165               | 1145   | 1014.5             | 961.5              | 906                | 887                | 806.5              | 778               | 758.5              | 754.5              | 729                | 724                | 723                | 703.5              | 697                | 683.5  | 674                | 669.5              | 657                | 643.5              | 640                | 640               | 621.5             | 598                | 595                | 595    | 587.5              |
| 17                 | 18     | 19                 | 20     | 21                 | 22                 | 23                 | 24                 | 25                 | 26                | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34     | 35                 | 36                 | 37                 | 38                 | 39                 | 40                | 41                | 42                 | 43                 | 44     | 45                 |

## ALIGNMENTS

1255

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YLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
 LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
 EGFR.
Rattus norvegicus (Rat).
Ebkaryota, Metazoa, Chodata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 "A truncated, secreted form of the epidermal growth factor receptor encoded by an alternatively spliced transcript in normal rat tissue. Mol. Cell. Biol. 10:2973-2982(1990).
 R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR000419; Euk_pkinase.
R InterPro; IPR0002174; Furin-like.
R InterPro; IPR0002174; Furin-like.
R InterPro; IPR001245; Furin-like.
R InterPro; IPR001245; Furin-like; I.
R Pfam; PF001039; Recept_L I.
R Pfam; PF001039; Recept_L I.
R PRINTS; PR00101; Euk_pkinase; I.
R PRINTS; PR00101; Euk_pkinase; I.
R PRODm; PR00119; FU; J.
R PROSITE; PS00101; PROTEIN KINASE DOM; I.
R PROSITE; PS00101; PROTEIN KINASE DOM; I.
R PROSITE; PS00109; PROTEIN KINASE TYP; I.
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 SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
Guttridge K., Dawson T.L., Earp H.S.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; M37334, ARF14008.1; -.
 databases
 SEQUENCE FROM N.A. STROMENTALE STRAINS TO STROME STRAINS TO SUBSECT TO STROME STRAINS STROME
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
 Petch L.A.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
 $
 1209
 SEQUENCE FROM N.A.
STRAIN-FISHER; TISSUE-LIVER;
 PRELIMINARY;
 NCBI_TaxID=10116;
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 ELTYLPTNASLSFLQDIQEVQGYVLIAHNOVROVPLORLRIVRGTQLFEDNYALAVLDNG
 DPLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 PSGVKPDLSYMP1WKFPDEEGACQPCP1NCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESIPPRRFT
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 IQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 1 LLVVVLGVVFG1 L1 KRRQQKI RKYTMRRLLQETELVEPLTPSGAMPNQAOMR 1 LKETEL
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYVMAGVGSP
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRRFT
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 Gaps
 . 9
 Length 1259,
 60; Indels
 . 9
 OB
 ; Score 6253; DE; Pred. No. 0; 40; Mismatches
 91.8%;
91.6%;
Query Match 91.8 Best Local Similarity 91.6 Matches 1154; Conservative
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PRELIMINARY;
 Mus musculus (Mouse)
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 NIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL 419
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 CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC 299
 CPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP-LISIVSAV 658
 651
 15 LAALCAAG-----GALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLE
 PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSA
 LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD
 TLIDTNRS-RACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ
 VGILLVVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKE
 PLNNOYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL
 VPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQE
 CVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVAR
 PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCS
 PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
 TELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGV
 DVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRR
 898 RFTHOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVK
 CWMI DSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGD
 LVDAEEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA
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1135 PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENP 1194
 EYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP----PERGAPPSTF
 1136 EYLNTAQ-----PTCLSSGFDSSALWIQKGSHQMSLDNPDYQQDFFPKEAKPNGIF
 SEQUENCE FROM N.A.
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threaddill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubzamaniam S., Crossley T.O., Magnuson T.R., James C.D.,
 STRAIN=CS7BL/6J;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D., Maihle N.J.;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 "Comparative genomic sequence analysis and isolation of human on mouse alternative Egfr transcripts encoding truncated receptor
 "Comparative genomic sequence analysis and isolation of human mouse alternative Egfr transcripts encoding truncated receptor
 isoforms.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275366; AAGZ8045.1; -.
EMBL; AF275364; AAGZ8045.1; JOINED.
EMBL; AF275365; AAGZ8045.1; JOINED.
EMBL; AF275365; AAGZ8045.1; JOINED.
EMBL; AF275365; AAGZ8045.1; -.
HSSP; P11362; 1FGK.
 Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UIN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor isoform 1.
 MOSITE F11362, IFGK.

MOSIS MGI:95294, EGFL.

InterPro; IPR000345; CytC_heme_bind.

InterPro; IPR000494; EGFR. domain.

InterPro; IPR00139; EUK_pkinase.

InterPro; IPR002174; Furin-like.

InterPro; IPR001296; Ser_thr_pkinase.

InterPro; IPR001296; Ser_thr_pkinase.

Pfam; PF001057; Furin-like; 1.

Pfam; PF001030; Recep_L_domain; 2.

Pfam; PF001030; Recep_L_domain; 2.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SWART; SM00220; TYRK; 1.

PROSITE; PS00109; TYRK; 1.

PROSITE; PS00109; TYRC; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
 1210 AA
 || || || || || || || 187 || 1202
 KGTPTAENPEYLGLDVP 1254
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1081

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1140 VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-T 1198
957 ADSRPKFRELILEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMEDVVDAD 1016
 1093 VNQ-SVPKRPAGSVQNPVYHNQPLHP------APGRDLHYQN--PHSNAVGNPEYLNT
 1199 PQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPPSTFKGTPT
 1142 AQ------PTCLSSGFNSPALWIOKGSHOMSLDNPDYQODFFPKETKPNGIFKG-PT
 EYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEGA
 ----SRTPLLSSLSA
 1082 GSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQPEY
 Xiphophorus xiphidium.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
 [1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE=898341172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock C., Gomez A., Duschl Altschmied J., Schartl M.;
"Activation of the Xmrk proto-oncogene of Xiphophorus by Overexpression and mutational alterations.";
 PERMIT PRO1000; Recep_L'domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM: PD000001; Euk_pkinase; 1.
SMART; SM00219; FU; 3.
SMART; SM00219; TYRKc; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00137; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE TAP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 2.
PROSITE; PS00101; PROTEIN KINASE TYP; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 the EMBL/GenBank/DDBJ databases
 Last sequence update)
Last annotation update)
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 PRT; 1165 AA
 Receptor tyrosine kinase proto-oncogene.
 Created)
 Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L domain;
 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
 1243 AENPEYLGLDVP 1254
 1192 AENAEYLRVAPP 1203
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 STRAIN=RIO PURIFICATION;
 Schartl M.;
Submitted (JUL-2000) to
 1017 EYLTPOOGFF----
 SEQUENCE FROM N.A.
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 -YGTNRTGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL--- 180
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 - SHPSSCPKCDPSCPNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG 239
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 896
 | SDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMVKGWMID 962
 SDVMSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIMVKCWMID 956
 ASLSFLQDIQEVQGYVLIAHNOVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNQYI 128
 FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLS 423
 664 VVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRK 722
 73
 KANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI
 LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQE
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 604 VKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILL
 VKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYVMAGVGSPYV
 11 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
 Gaps
 45.9%; Score 3128; DB 11; Length 1210;
llarity 49.5%; Pred. No. 4.2e-227;
Conservative 170; Mismatches 362; Indels 110;
 134840 MW; 62CD021C9DE32E18 CRC64;
 ATP-binding; Receptor; Transferase
 1210 AA;
 Similarity
 Best Local Simi
Matches 630;
 SEQUENCE
 69
 125
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 244
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 364
 359
 424
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1176 GKNGVVKDVFAFGGAVENPEYLIPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPS 1235
 1010 EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEE 1069
 161 LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC 220
 ---EPCIPPNGH---------PVRENSIALRYISDPTQNALEKDLDGH-
 1129 APLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSP
 1070 APRSPLAPSEGAGSDVFDGDLGMGAAKGLOSLPTHDPSPLORYSEDPTV-PLPSETDGYV
 Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
 77; Gaps
 Query Match 40.1%; Score 2729.5; DB 13; Length 1137; Best Local Similarity 47.3%; Pred. No. 4.8e-197; Matches 539; Conservative 169; Mismatches 354; Indels 77; C
 11
 -----RYKRIN-ROGS----
 Dixon M., Lumsden A.;
"Distribution of neuregulin-1 (nrgl) and erbB4 transcripts
"Distribution of neuregulin-1,";
mbryonic chick hindbrain.";
Mol. Cell. Neurosci. 13:237-258(1999).
EMBL; AF121963; AAD31764.1; -.
HSSP; P11362; 1FGK.
 1137 AA; 127927 MW; 4D616436F87DC84F CRC64;
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 $
 R InterPro; 1F00019; Euk_Dkinase.
R InterPro; 1F00019; Euk_Dkinase.
R InterPro; 1F000114; Furin-like.
R InterPro; 1F000114; Furin-like.
R InterPro; 1F0001245; TVr Dkinase.
R InterPro; 1F0001245; TVr Dkinase.
R InterPro; 1F0004019; VVr Dkinase.
R Pfam; PF00103; Recep_L_domain; 1.
R Pfam; PF00103; Recep_L_domain; 1.
R Pfam; PF00103; TVRKINASE.
R SMART; SM00109; TYRKINASE.
R SMART; SM00109; TYRKC; 1.
R PROSITE; PS00109; PROTEIN KINASE ATP; 1.
R ROSITE; PS00109; PROTEIN KINASE TYR; 1.
R ROSITE; PS00109; PROTEIN KINASE TYR; 1.
R ROSITE; PS00109; PROTEIN KINASE TYR; 1.
R RNOSITE; PS00109; PROTEIN KINASE TYR; 1.
R ROSITE; PS00109; PROTEIN KINASE TYR; 1.
R RNOSITE; PS00109; PROTEIN KINASE TYR; 1.
R RNOSITE; PS00109; PROTEIN KINASE TYR; 1.
 1137
 995 SSDD--DVVDADEYLL------
 Receptor tyrosine kinase (Fragment)
ERBB4.
 SEQUENCE FROM N.A.
TISSUE=HINDBRAIN;
MEDLINE=99263203; PubMed=10328884;
 1236 TFKGTPTAENPEYLGL 1251
 PRELIMINARY;
 Gallus.
NCBI_TaxID=9031;
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 DVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLL 1009
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 FGASCYTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHL 350
 SNTIAVNSTNIGSFSNCTKINGDIILNRNSFEGDPHYKIGPMDPEHLMNLTTVKEITGYL 407
 469
 589
 580
 649
 709
 769
 889
 949
 467
 638
 697
 757
 829
 877
 99
 4 LELLEL----LLLLLSIGRCCSTDPDRKVCQGTSNQMTM---LDNHYLKMKKMYSGCNV
 LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT
 56 VQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALA
 116 VLDNGDPLNNQYIKANSK----FIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKD
 REVRAVTSANIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYL
 411 YISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIH
 530 NCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAH
 1 MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
 172 IFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGP
 470 HNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCV
 590 YKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRAS
 581 FQDGPQCIPRCPHGMLGDGDTL-IWKYADKMGQCQPCHQNCTQGCSGPGLSGCRGD-IVS
 AQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILD
 AKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWM
 EAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQI
 Gaps
 Indels 148;
129614 MW; 7F7EE38D8771A74E CRC64;
 ch 40.4%; Score 2749; DB 13; al Similarity 45.8%; Pred. No. 1.7e-198; 584; Conservative 162; Mismatches 382;
A.
 Query Match
Best Local Similarity
1165
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 PLPAA-RPAGATLERAKTLSPGKNGVVKDVF-----AFGGAVENPEYLTPQGGAAPQ 1206
 1011 DLQAVDNPEYHN-----APNGQPKAEDEYVNEPLYLNTFANTLENAEYL------K 1055
 806
 998
 PHPPPAFSPAFDNLYYWDQDPPERGA--PPSTFKGTPT-------AENPEYL 1249
 279
 459
 477
 61
 VVIQNED-LGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHH
 CWGPGPDQCLSCKRFIRGRTCIESCNLYDGEFREFANGSVCMECDPQCEKMEDNMITCYG
 DKGC------PAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYT
 CLEHNHNAKYTYGAFCVKKCPHNFV-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICP
 SHDCIYYPWTRQSTLPQHAR-TPL--IAAGVIGGLFIIVIMGLTFAVYVRRKSIK-KKRA
 RHRSSSTRSGGGDLTLGLEPSEEEAPRS--PLAP-SEGAGSDVFDGDLGMGAAKGLQSLP
 ESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCA
 FETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLR
 ELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGH
 CWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFG
 PEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLD
 KI PVAI KVLRENTS PKANKE I LDEAYVMAGVGS PYVSR LLGICLTSTVQLVTQLMPYGCL
 LDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGL
 ARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGI
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LVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVP-QAFNIPPPIYTSRTRIDS
 THDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG
 RVCYGLGMEHLREVRAVTSANIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQV
 MRRILQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENV
 180
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NNLPEKAKKAFDNPDYWNHSLPPRSTLQHPDYLQEYSTKYFYKQNGRIRPIVAENPEYL 1114
 301
 343
 420
 62
 63
 9 WGLLLALLPP--GAASTQ----VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEL
 TYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP
 LNNQYIKANSKFIGITELOLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALT
 ----YPKDGPS--GLNQLGLMNLTEILDGGVQIINNKYLRYGPWVYWRDII-RNNDAPIE
 LIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCA
 AGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPY
 AGCKGPLDTDCFACRLFNDSGACVPQCPQTLIYNKQTFQMETNPNAKYQYGSICVSQCPT
 HEV-VDGSSCVSVCPPDKMEV--ERGSQRQCELCSGLCPKVCEGTGAE---QRQTVDSSN
 NYLSTDVGSCTLVCPLHNQEVTAEDGTQR-CEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 Gaps
 Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
 Length 1328,
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 wnt1 locus
 Indels
 01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 SMART; SM00261; FU; 3.
SMART; SM00219; TYrKC; 1.
SMART; SM00109; TYRKC; 1.
PROSITE; PSS00101; PROTEIN KINASE ATP; 1.
ATP-binding; Transferase.
SEQUENCE 1328 AA; 148613 MW; A333039258B647E9
 Best Local Similarity 40.6%; Pred. No. 1.2e-165; Matches 522; Conservative 155; Mismatches 419;
 DB 13;
 34.0%; Score 2315; DB 13; 40.6%; Pred. No. 1.2e-165;
 DNA around the
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 1328
 EMBL, AF056116; AAC34391.1; HSSP, P11362; 1FGK.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR00119; Euk pkinase.
InterPro; IPR01245; Tyr pkinase.
Ffam; PF00157; Furin-like; IPFam; PF00169; pkinase; IPFam; PF00109; Recep L domain; 2.
ProDom; PD000001; Euk pkinase; I
 SEQUENCE FROM N.A.
MEDLINE-29177347, PubMed=10077531;
Melliner K., Brenner S.;
"Analysis of 148 kb of genomic DNA
 rubripes.";
Genome Res. 9:251-258(1999)
 PRELIMINARY;
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NCBI_TaxID=7165;
 Lycett G.J.;
 STRAIN=SUA;
 Receptor.
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 YMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLED 1011
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 CVEECRVLQGLPREYVNARH-CLPCHPECQPQNGSVTCFGPEADQCVACAHYXDPPFCVA
 LSMGSLDHPYIVRLLGICPGTCLQLVTQLSSHGSLLEHIRQHKTSLDPQRLLNWCVQIAK
 -----GILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQ
 ESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDV
 1012 DOMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP
 - FAVSQGGHIGYLPMSPSPVDTIRQLWYQRSRLSSVRTLPDRSAFRRSSREAELCEDGAQ
 1104 CAGIFRVR-------FGSERGN-----PQGG------
DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPH-QALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQE
 RCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAV
 640 TGIALGVPAGLIFCLVLFFLGMLYHRGLAIRRKRAMRRYLESGESFEPLGP-GEKGTKVH
 MRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEA
 772 YVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAK
 GMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMAL
 ------RYSEDPTV
 -----GLGDRFATPSLQPSPSWSTSPSQINSYMVMTQLRYD----
 1119 PLPSETDGYVAPLTCSPQP-EYVNQ-------PDVRPQPPSPREGPL--PAAR
 1162 PAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLY
 Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 09BIH9 PRELIMINARY; PRT; 1433 AA. 09BIH9; 01-JUN-2001 (TEMBLrel. 17, Created) 01-JUN-2001 (TEMBLrel. 17, Last sequence update) 01-JUN-2002 (TEMBLrel. 17, Last annotation update) Putative epidermal growth factor receptor (Fragment) EGFR.
 1072 RSPLAPSEGAGSDVFDGDLGMG---AAKGLQSLPTHDPSPLQ-
 --QORKLSTASSPSSFKTWAADEEDE 1146
 1222 YWDQDPPERGAPPSTFKGTPTAENPE 1247
 VGILLWWLGWF-
421
 669
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 GKMPQNSE-----CVPCKGVCPKTCPGEGIVH-----SDNIGNYKDCTIIEGSLEIL 329
 429
 389
 488
 449
 548
 206
 85
 9
 QLRSLTEILKGGVLIQRNPQLCYQDTILWKDI-FHKNNQLALTLIDTNRSRACHPCSPMC
 KGSRCWGESSEDCOSLTRTVCAGGCA--RCKGPLPTDCCHEOCAAGCTGPKHSDCLACLH
 86 IAHNOVROVPLORLRIVRGTQLF----EDNYALAVLDNGDPLNNOYIKANSKFIGITEL
 FNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPL
 26 CTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVL
 318 HNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFL
 378 PESFDGDPASNT-----APLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQ
 430 VIRGRILHNGAY-SLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRN
 SDHEVWYQKNRNATECHEEGMECSEQCSKAGCWGKGPEQCLECKNVKYKGKCLDSCK---
 PHQALLHTANR PEDECVGEGLACHOLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQ
 Gaps
 Indels 385;
 Length 1433;
 and localisation of the Anopheles gambiae
 T "Cloning, expression and localisation of the Anopheles gamb epidermal growth factor receptor.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

R HSSP, p1362; LRGX.

R InterPro; IPR000349; CQCC heme bind.

R InterPro; IPR000494; EGFR_L domain.

R InterPro; IPR000494; EGFR_L domain.

R InterPro; IPR000199; EGFR_L domain.

R InterPro; IPR002109; Ser_L hr_ pkinase.

R InterPro; IPR002104; Furin-1ike.

R InterPro; IPR001245; Tyr_ pkinase.

R InterPro; IPR001245; Tyr_ pkinase.

R Efam; PF00109; PYRKINSE.

DR PF00109; PYRKINSE.

DR PR00109; PYRKINSE.

DR SWART; SW00220; STRC; 1.

DR SWART; SW00220; TYCC; 1.

DR SWART; SW00219; TYCC; 1.

DR PROSITE; PS001007; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS001007; PROTEIN_KINASE_TYR; 1.
 1433 AA; 159585 MW; E3D9D88967724F07 CRC64;
 Query Match
30.1%; Score 2047.5; DB 5;
Best Local Similarity 32.7%; Pred. No. 2.2e-145;
Matches 473; Conservative 196; Mismatches 393;
SEQUENCE FROM N.A.
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 |:::|:|:| | :|||| | ||::||| |:: ||::|:: || |::| |::| |::| AKDVPELIEIGHKLPQPDICSLDVYCILLSCWVLDADARPTFKQLAETFAEKARDPGRYL 1101
 MI------PGDKFMRLPSYTNQDEKDLIRTLAPVAMAAAAAAAAAAAGASNVDVPSTIA 1152
 -PLAP---SEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVA 1129
 PLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGG 1189
 747
 807
 867
 AREIPDLLEKGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFV 987
 621
 621
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 801
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 981
 RLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIP 927
 681
GLPREY-VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP-----
 TMALAGCEDSEPLRPSNVGPNLTKLRIIKEAEIRRGGVLGMGAFGRVFKGVMMPEGESVK
 IPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLL
 ||||||||||| | : ::|| |:|||:||| | : :|| :|| :|| :|| ||| ||| ||| ||| ||| IPVAIKVLMEMSGSESSKEFLEEAYIMASVEHPNLLKLLAVCMTSQMMLITQLMPLGCLL
 DHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLA
 988 VIONEDLGPASPLDSTFYRSLLEDDDMGDLV--------
 1019 DAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRS----
 SLPRLYSVDSKTCGDCHQECKD-----FCYGPNEDNCGSCMNVKDGRFCVAECPTTKHAM
 QEEGPLKQLSGKAVCRKCHPRCKKCTGYGFHEQFCQECTGYKKGEQCEDECPQDFYANEE
 --------RASPLTSIVSAVVGILLVVVLGVVFGI----LIKRRQQKIRKYTM
 GKIGPYCSADSMQSGLRIEPQTQVKIVMGSVMALILLCVVFGIAFVLFSRHKNKKDAVKM
 P-TCQSQ----TPG----YMDLIGVPA
 1190 AVENPEYL-----TPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGT
 RRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
 562 NGTCINCHKTCVGCRGPRDTIAPDGCISCDKAIIGSDAKIERCLMKDESCPDGYYSDYVL
 --ACQPCPINCT-----HSCVDL-----DD------KGCPAEQ-----
 Created)
Last sequence update)
Last annotation update)
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 419
 PRT;
 (TrEMBLrel. 13, (TrEMBLrel. 16, 1) (TrEMBLrel. 21, 1)
 PRELIMINARY;
 PTAENPE 1247
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PTHQHSQ 1287
 Q9UK79;
01-MAY-2000 (
01-MAR-2001 (
01-JUN-2002 (
Herstatin.
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 241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNFGRYTFGASCVTACP
 DPLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 Gape
 Henner W.D.;
 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Euteleostomi;
 n G.M.;
secreted
 .;
 26.4%; Score 1798.5; DB 4; Length 419; 86.5%; Pred. No. 2.2e-127;
 MEDLINE=99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.
TTHe HER-Z/neu receptor tyrosine kinase gene encodes a secautoinhitor "
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 39; Indels
 Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., He Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF17761, AAD56009.2; -.. InterPro; IPR000494; EGFR. L. domain. InterPro; IPR00174; Furin-like. Pfam; PF001037; Furin-like; J. Pfam; PF01030; Recep L. domain; J. SMART; SM00261; FU; T.
 the EMBL/GenBank/DDBJ databases
 45472 MW; FEC1BE347E2D030C CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
 Pred. No. 2.2e-127; 7; Mismatches 39;
 387
 361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQP 394
 LRMQPG - - PAHPVLSFLRPSWDLVSAFYSLPLAP
 367
 Best Local Similarity
Matches 341; Conservative
 PRELIMINARY;
 Strausberg R.;
Submitted (APR-2002) to
(Human)
 419 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=9606;
 autoinhibitor
 181
 301
 121
 181
 241
 356
 SEQUENCE
 Query Match
 Q8R2X1
 Q8R2X1
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15;

628

687

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807

373

253

927

867

seq4-103-117-12.rspt

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988 VIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHR 1046
 1102 PTHDPSPLORYSEDPTVPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPA 1159
 1047 HRSSSTRSGGGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSL 1101
 599 -NSPST------RNGQGH 631
 928 AREIPOLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFV 987
 NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVVLGVVFGILIKRRQQKIRKYTM
 DHVRENRGRLGSQDLLNWCMQI AKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLA
 868 RLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIP
 569 PONGSVICFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
 RRLLOETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
 IPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLL
 Gaps
 with
 1160 ARPAGATLERAKTLSPGKNGVVKDVF------AFGGAVENPEYL 1197
 676 -----TAMVQNQIYNNISLTAISKLPMDSRYQVSHSTAVDNPEYL 715
 Indels 102;
 Length 729;
 Avian rous-associated virus type 1.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11950;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 25.3%; Score 1720; DB 15; 54.8%; Pred. No. 4.3e-121; iive 75; Mismatches 118;
 EMBL; S69372; AAC60727.1; --
HSSP; P11362; 1FGK.
InterPro; IPR000719; Euk pkinase.
Query Match
Best Local Similarity 54.8%
Matches 358; Conservative
 V-erbB protein (Fragment).
 PRELIMINARY;
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 APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG 1188
 ö
 948
 61 IDVYMIMVKCWAIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPSSPMDSTFYRSL 120
 9
 1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
 949 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
 181 EPPRSPLAPSEGAGSDVFDGDLAVGVTKGLQSLSPHDLSPLQRYSEDFTLPLPPETDGYV
 889 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
 LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEE
 EAPRSPLAPSEGAGSDVPDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
 GAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEY
 SEQUENCE FROM N.A.
MEDLINE=94203659; PubMed=8152791;
Wennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene sequences: rapid
evolution of distinct viral genomes carrying mutant v-erbB genes with
different transforming capacities.";
 Gaps
 ö
 Length 367;
 InterPro; 1PR004038; Retro M.
InterPro; 1PR004038; Retro M.
InterPro; 1PR001038; Retro M.
InterPro; 1PR001038; Retro M.
InterPro; 1PR001045; Tyr_pKinase.
Pfam; PF02813; Retro M; 1.
Pr050m; PF02813; Retro M; 1.
Pr050m; PF00107; PR07EIN_KINASE ATP; 1.
PROSITE; PS00107; PR07EIN_KINASE DOM; 1.
PROSITE; PS00109; PR07EIN_KINASE_TYR; 1.
PR05ITE; PS00109; PR07EIN_KINASE_TYR; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 729 AA; 80649 MW; 84D2F6914FFEID63 CRC64;
 %; Score 1739; DB 11; Length
%; Pred. No. 5.7e-123;
11; Mismatches 33; Indels
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Polyprotein.
PolyPROTEIN.
Avian rous-associated virus type 1.
Avian rous-associated virus type 1.
 40163 MW; OBE03395F9E101B0 CRC64;
 25.5%;
 EMBL; S69372; AAC60725.1; -. HSSP; P03322; 1A6S.
 BC027080; AAH27080.1;
 Query Match
Best Local Similarity 88.0°
Matches 323; Conservative
 PRELIMINARY;
 LGLDVPV 1255
 Hypothetical protein. SEQUENCE 367 AA; 4
 361 LGLDVPV 367
 NCBI_TaxID=11950;
 1009
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 1129
 241
 1189
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EMBL;
 086712
 086712
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 1056 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110
 969
 491
 637
 756
 173
 233
 876
 293
 936
 353
 526
 57
 578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
 GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL
 ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
 LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE
 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
 294 YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE
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 RYSEDPTVPLPSET - - DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE
 1 GP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP
 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Indels 102;
 Length 567;
 RAKTLSPGKNGVVKDVF-----AFGGAVENPEYL 1197
 999
 567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
 ----TAMVONOIYNNISLTAISKLPMDSRYONSHSTAVDNPEYL
 QBWYVO;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
 / Match 25.2%; Score 1718; DB 15;
Local Similarity 55.4%; Pred. No. 4.2e-121;
Nes 357; Conservative 73; Mismatches 112;
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRNINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TYRK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
TYCOSITE; PS00109; PROTEIN KINASE_TYR; 1.
 PRT;
 PRELIMINARY;
 Homo sapiens (Human)
 638
 174
 1169
 SEQUENCE
 58
 817
 877
 1111
 Query Match
 455
 527
 QBWYVO
 Best Lock
 RESULT 12
 Q8WYVO
ID Q8
AC Q8
AC Q8
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1128
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 -----HPPPA---FSPAFDNL 1220
 120
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 1069 EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLOSLPTHDPSPLQRYSEDPTVPLPSETDGYV
 1129 APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPCKNGVVKDVFAFG
211 APLTCSPQPEYVNQPDVRPQPPSFREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFG
 61 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
 1009 LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
 121 LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
 301 GAVENPEYLTPQGGAALSPTLLLPSAQPSTTSITGTRTHQSGGLHPAPSKGHLRQRTQST
 949 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
 Gaps
 MEDLINE=90206603; PubMed=1969616;
Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
"Six amino acids from the retroviral gene gag greatly enhance the
transforming potential of the oncogene v-erb-B.";
 SEGUENCE FROM N.A. Hang P.P., Jiang H.Q., Qin W.X., Zhao X.T., X. Zhou X.M., Zhou X.M., Zhou X.M., Zhou X.R., Wan D.F., Gu J.R.; "Novel human cDNA clones with function of inhibiting cancer cell
 53;
 410
 4; Length 412;
 1221 YYWD-QDPPER-----GAPPSTFKGTPTAEN
 22; Indels
 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF318349; AAL55856.1; -.
InterPro; IPR000748; EP-hand.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00145; Tyr_pkinase.
InterPro; IPR00145; Tyr_pkinase.
InterPro; IPR00169; YLP_motif.
Pfam; PF00069; pkinase; I.
ProDom; PF007057; Uk, pkinase; I.
SMART; SM00219; TyrKC; I.
 1 protein.
412 AA; 44702 MW; 034397FF3F27D2BC CRC64;
 U
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 Avian type
 24.9%; Score 1697.5; DB 4; 80.5%; Pred. No. 9.2e-120; ive 5; Mismatches 22;
 PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11861;
 GAVENPEYLTPOGGAAPOP
 Gag, v-erb-A, v-erb-B protein.
GAG, V-ERB-A, V-ERB-B.
 Query Match
Best Local Similarity 80.51
Matches 330; Conservative
 PRELIMINARY;
 [1]
SEQUENCE FROM N.A.
NCBI_TaxID=9606;
 Hypothetical
 growth.";
Submitted
 1189
 SEQUENCE
 064895;
 064895
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1107 SPLORYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT 1166
 RN (1)

RN SEQUENCE FROM N.A.

RA SCOtting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.;

RA Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.;

RT "Common site of mutation in the erbB gene of avian erythroblastosis

RT "Common site of mutation in the erbB gene of avian erythroblastosis

RT Orcogene Res. 1:265-278(1987).

REMBI: X06943; CAA30024.1; -.

RESP: P1136.2 1FGW.

RISP: P1136.2 1FGW.

RISP: P1136.2 1FGW.

RISP: P1136.2 1FGW.

RIANE: PRO0179; Euk pkinase.

RIANE: P00000001; Euk pkinase.

REMBI: P00000001; Euk pkinase.

REMBI: P00000001; Euk pkinase.

REMBI: P00000001; PROTEIN KINASE DOM; 1.

RROSITE; PS00101; PROTEIN KINASE TYR; 1.

RROSITE; PS00101; PR0TEIN KINASE TYR; 1.
 578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
 S8 GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL
 ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
 YHADGGKVPIKWMALESILRRRFTHOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
 KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG
 LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE
 638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
 VEPLTPSGAMPNOAOMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
 92; Gaps
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-erbB gene.
Avian erythroblastosis virus (Ts34) v-erbB gene.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 Indels
 Query Match
24.2%; Score 1645; DB 15;
Best Local Similarity 54.9%; Pred. No. 1.3e-115;
Matches 345; Conservative 70; Mismatches 121;
 -LERAKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
 937 AISKLPMDSRYQN-----SHSTAVDNPEYL 961
 $
 545
 PRELIMINARY;
 1167
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 HRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDP 1106
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 AREIPDLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFV 987
 NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM
 RRILQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
 C----CHPECQ
 RLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIP
 PONGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
 IPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLL
 DHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLA
 Gaps
Oncogene 5:15-24(1990).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL; X52209; CA336459.1; -.
EMBL; X52219; CA336459.1; OINED.
HSSP; P10828; 2NLL.
 Probom; P000001; Zuf_Cateroid; 1.

Probom; P0000015; Zuf_Cateroid; 1.

SMART; SM00419; HOLI; 1.

SMART; SM00319; Zuf_Cat.

SMART; SM00319; Zuf_Cat.

PROSITE; PS00101; MUCLEAR_RECEPTOR; 1.

PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

ATP-binding; DNA-binding; Nuclear procein; Receptor; I.

ATP-binding; DNA-binding; Nuclear procein; Kinase; I.

Transcription regulation; Transferase; Tyrosine-protein kinase;
 24.3%; Score 1653.5; DB 15; Length 962; 51.7%; Pred. No. 6.9e-116; ive 73; Mismatches 142; Indels 119;
 962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
 InterPro; IPR000719; Euk pkinase.
InterPro; IPR000719; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmu-receptor.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
 541 VEECRVLQGLPRE-YVNAR-HCLP-----
 PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
 -NSPST-----
 Matches 358; Conservative
 Similarity
 Zinc-finger
 569
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PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1055
 .111 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1169
 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STAIN-CSTBL/GB, STAIN-CSTGL/GB, STAIN-CST
 -------PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQIQIYNYISLTAISK 523
 ---NSPST---
 STRAIN=C3H1101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J. Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D., Maihle N.J.;
 "Alternative Transcripts from the Human and Mouse EGFR Genes Encode Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
 STRAIN-C57BL/6J; TISSUE=LIVER;
Reiter J.L. Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.
Maihle N.J.;
 "Comparative genomic sequence analysis and isolation of human
 mouse alternative Egfr transcripts encoding truncated receptor
 Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
 414 LPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFF-----
 1170 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
 655
 PRELIMINARY;
 musculus (Mouse).
 SEQUENCE FROM N.A.
 [2]
SEQUENCE FROM N.A.
 Hayashizaki Y.;
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 - SHPSSCPKCDPSCPNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG
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 304 LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQE
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 CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
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 424 VFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD
 QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE
 CRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSG
 LLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
 74 YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN-----
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 23; Gaps
full-length mouse cDNA collection.";
 655;
 Length
 Query Match 22.3%; Score 1519.5; DB 11; Lengt
Best Local Similarity 44.0%; Pred. No. 5.1e-106;
Matches 281; Conservative 100; Mismatches 235; Indels
 72906 MW; 6B34063B1BC928CB CRC64;
 604 VKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC
 Nature 409:685-690(2001).
EMBL; AF12413; AD44149.1;
EMBL; AF275366; AAG28047.1;
EMBL; AF275364; AAG28047.1;
EMBL; AF275365; AAG28047.1; JOINED.
EMBL; AK004944; BAB23688.1;
EMBL; AK004941; BAB23681.1;
EMBL; AK004911; BAB23662.1;
 InterPro; IPR000494; EGFR L domain.
InterPro; IPR002174; Furin-like.
Pfam; PF00157; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
SMART; SM00261; FU; 3.
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 655 AA;
 MGD; MGI:95294;
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(without alignments)
4403.399 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDS2/gcgdata/geneseqf/geneseqp-embl/AA1991.
 1 MELAALCRWGLLLALLPPGA.......TFKGTPTAENPEYLGLDVPV 1255
 July 22, 2003, 08:11:38 ; Search time 37.9774 Seconds
 908470
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 908470 segs, 133250620 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 SEQ4-103-117-12
6809
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |            |        | Description         | Human herequlin 2 | Human tyrosine kin | HER2 transgene pla | Human HER2 (ErbB2) | HER-2/neu protein. | Human HER-2/neu on | Human HER-2/neu pr | Amino acid segment | Human HER-2/neu pr | HER2/neu amino aci |
|-----------|------------|--------|---------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| COMMAKIES |            |        | ID                  | AAY92620          | AAE12130           | AAB60167           | AAU74545           | AAW01111           | AAW92406           | AAB21198           | AAY84780           | AAB85458           | AAG88267           |
|           |            |        | 80                  | 21                | 22                 | 22                 | 23                 | 17                 | 20                 | 21                 | 21                 | 22                 | 22                 |
|           |            |        | e Match Length DB I | 1255              | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               |
|           | <b>a</b> p | Query  | Match               | 98.9              | 98.9               | 98.9               | 98.9               | 98.8               | 98.8               | 98.8               | 98.8               | 98.8               | 98.8               |
|           |            |        | Score               | 6736              | 6736               | 6736               | 6736               | 6730               | 6730               | 6730               | 6730               | 6730               | 6730               |
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| Her-2 produced to the control of the control of control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Human prog<br>Human prog<br>Human proj                                 | xic T-lymphocyte immunity; prostate cancer; gn epitope.  on oreign epitope insertion" oreign epitope insertion" on oreign epitope insertion" on oreign epitope insertion" on                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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E<br>n; forei<br>fiers<br>inal<br>polypep<br>ion regi<br>lion regi<br>lion regi<br>lion regi<br>lion regi                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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| 3083<br>3083<br>3083<br>3083<br>3083<br>3083<br>3083<br>92620<br>92620 | Human heregul<br>Heregulin 2;<br>self-protein;<br>cell-associat<br>Homo sapiens.<br>Key<br>Domain<br>Region<br>Region<br>Region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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 This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a response. Subdominant CTL epicopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign helper epitopes were identified (see features table). The method
 Dalum
 tumor associated
prostate cancer
 /label= insertion region
/note= "suitable for foreign epitope insertion"
1011..1235
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 Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
 /label= Tyrosine_kinase_domain
661..675
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 324..483
/label= Ligand_binding_domain
 'label= Cysteine_rich_domain
 'label= Cysteine_rich_domain
 'label= Transmembrane_domain
 /label= C-terminal_domain
 Claim 62; Page 193-198; 220pp; English.
 Nielsen KG,
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Karlsson G;
 98DK-0001261.
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 184..623
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 WPI; 2000-349917/30
 Birk P,
 N-PSDB; AAA09455
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (FA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (FSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (AFCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 if irst T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial PA and including at least to the animal epitopes of the respective PA and including at least to reside the past of the respective PA and including at least to reside the present of the past of the respective method is used to treat prostate, prostate/breast or breast cancer.
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 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTVNTDTFESMPNPEGRYTFGASCVTACP
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DPLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWGPGPTOCVNCSQFLRGQEC
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMP1WKFPDEEGACQPCP1NCTHSCVDLDDKGCPAEQRASPLTS1VSAVVG
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVA I KVLRENTSPKANKE I LDEAYVMAGVGSP
 Gaps
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0
 DB 21; Length 1255;
 Indels
 The method is used to treat prostate, prostate/breast o
when the PA is human PSM, FGF8b and Her2, respectively.
 10;
 98.9%; Score 6736; D
99.0%; Pred. No. 0;
iive 2; Mismatches
 Matches 1243; Conservative
 1255 AA;
 Similarity
 541
 Sequence
 121
 181
 241
 301
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 481
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 181
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 421
 481
 541
 601
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 661
 661
 Query Match
 721
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EEYLVPQQGFFCPDPAPGAGGWHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 EEYLVPQQGFFCPDPAPGAGGWVHRRRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG
 Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
 Therapeutic compound, major histocompatibility complex, vaccine, antigenic peptide, MHC; immunoregulatory; immune response, HER-2; adoptive immunocherapy; anti-cancer; breast cancer antigen; APC; antigen presenting cell; human; tyrosine kinase-type receptor.
 Human tyrosine kinase-type receptor, HER-2,
 Location/Qualifiers
774..782
/note= "Antigenic epitope"
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 standard; Protein; 1255
 16-MAR-2001; 2001WO-US40328
 16-MAR-2000; 2000US-0527487
 2001-616284/71
 N-PSDB; AAD19731.
 GENZ) GENZYME
 WO200168677-A2
 Nicolette CA;
 sapiens
 20-SEP-2001
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducting an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides inch obser cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
 180
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 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
 360
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 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
 DPLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNFEGRYTFGASCVTACP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 Gaps
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 Length 1255
 Indels
 10;
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 Query Match
98.9%; Score 6736; D
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1243; Conservative 2; Mismatches
 Claim 4; Page 63-67; 69pp; English
 1255 AA;
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The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQCCQVVQGNL
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYVMAGVGSP
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 Length
 Indels
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 10;
 DB
 98.9%; Score 6736; Dilarity 99.0%; Pred. No. 0; Conservative 2; Mismatches
 2;
English
92pp;
 Query Match
Best Local Similarity
Matches 1243; Conserv
 1255 AA;
Fig 4;
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 181
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 541
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 Sequence
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 ErbB
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG
 EEYLVPQQGFFCPDPAPGAGGMVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 which overexpress an antibody, comprises
 conjugate;
 maytansinoid
 construct encoded protein.
 Treating tumors, particularly breast cancers, receptor and does not respond to an anti-ErbB conjugating the antibody to a maytansinoid -
 receptor; pl85neu;
 Z
 Protein; 1255
 99US-0141316
2000US-0189844
 2000WO-US17229
 transgene plasmid
 (GETH) GENENTECH INC
 Schwal1
 WPI; 2001-061962/07.
N-PSDB; AAF24297.
 standard;
 ErbB2
 WO200100244-A2
 Human; HER2;
 23-JUN-2000;
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 sapiens
 25-JUN-1999;
16-MAR-2000;
 03-APR-2001
 04-JAN-2001
 Synthetic.
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ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
 is characterised by the overexpression of an epidermal growth factor receptor (BrbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, alivary alland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithalial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2)
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR 840
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDIFESMPNPEGRYTFGASCVTACP
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 DPLNNQYIKANSKFIGITELOLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGCARCKGPLPTDCCHEQC
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 ILLWWLGWFGILIKRROOKIRKYTMRRLLOETELVEPLTPSGAMPNOAQMRILKETEL
 DB
 Score 6736; DB
Pred. No. 0;
2; Mismatches
 2;
 polypeptide of the invention.
 98.9%;
99.0%;
 Best Local Similarity 99.0
Matches 1243; Conservative
 1255 AA;
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 Sequence
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 Query Match
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 Human; HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ovary; stomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; inflammatory disorder;
 The invention relates to treating a tumour in a mammal, where the tumour
 EEYLVPQQGFFCPDPAPGAGGMVHHRRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
 angiogenic disorder; immunological disorder
 Sliwkowski
 AAU74545 standard; Protein; 1255
 (ErbB2) polypeptide.
 3; Fig 7; 93pp; English
 16-MAR-2000; 2000US-189844P.
05-OCT-2000; 2000US-238327P.
 16-MAR-2001; 2001US-0811123
 (first entry)
 Schwall R,
 SLIWKOWSKI M.
 2002-163686/21.
 (ERIC/) ERICKSON S. (SCHW/) SCHWALL R.
 N-PSDB; ABK14058
 US2002001587-A1.
 sapiens
 23-APR-2002
 Erickson S,
 03-JAN-2002
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IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLY1SAWPDSLP
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 ILLVVVLGVVFGILIKRRQOKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 DPLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, overain, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
 Length 1255;
 Indels
 17;
 11;
 8
 Mismatches
 6730;
No. 0;
 Score (
 98.8%; Scc.
98.9%; Pred.
3; M
 Best Local Similarity 98.9
Matches 1241; Conservative
 1255 AA;
 361
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 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 676..1255 /
/label= Intracellular_domain
/note= "claimed domain, useful for immunisation"
 HER-2/neu; c-erbBl; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; immunisation; tumour; vaccine; vector.
 used for prevention
HER-2/neu oncogene i
 DNA encoding HER-2-neu poly:peptide(s) - treatment of malignancies with which the
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 Location/Qualifiers
 Claim 2; Page 56-61; 71pp; English
 AAW01111 standard; Protein; 1255
 96WO-US01689
 95US-0414417
 entry)
 (UNIW) UNIV WASHINGTON
 Disis ML;
 WPI; 1996-455361/45.
N-PSDB; AAT40739.
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 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
 B cell; immunisation;
 response
 Use of HER-2/neu polypeptides - for eliciting an immune respon
an HER-2/neu associated malignancy, particularly for treating
 /note= "region which elicits immune
 cell;
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 immune response;
 26pp; English
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 Location/Qualifiers
676..1255
 oncogene protein.
 AAW92406 standard; Protein; 1255
 malignancy; treatment; tumour.
 93US-0033644.
93US-0106112.
95US-0414417.
 96US-0625101
 96US-0625101
 entry)
 (UNIW) UNIV WASHINGTON
 Column 31-38;
 Disis ML;
 oncogene;
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 1999-152835/13.
0B; AAX01912.
 tumours
 17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
 Homo sapiens
 01-APR-1996;
 Cheever MA,
 21-APR-1999
 US5869445-A
 09-FEB-1999
 preventing
 HER-2/neu;
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 WPI, 1999
N-PSDB;
 Region
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This sequence represents the human HER-2/neu oncogene protein. A fragment

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of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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 ELTYLPTNASLSFLQDIQEVQCYVLIAHNQVROVPLQRLRIVRGTQLFEDNYALAVLDNG
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 1 MELAALCRWGLLLALLPPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 LTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 1LLVVVLGVVFG1LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMR1LKETEL
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTSPKANKEI LDEAYVMAGVGSP
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 .
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 Length 1255;
 20;
 11;
 ВВ
 Score 6730; DB
Pred. No. 0;
3; Mismatches
 3,
 98.8%;
 Best Local Similarity 98.9
Matches 1241; Conservative
 Sequence
 61
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 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960
 PSGVKDDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 MELAALCRWGLLIALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQCCQVVQGNL
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWGPGPTOCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 1 MELAALCRWGLILLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 DPLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVA I KVLRENTSPKANKEI LDEAYVMAGVGSP
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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 Length 1255;
 Indels
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 Mismatches
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Pred. No. 0;
 98.8%;
98.9%;
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Matches 1241;
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 IDSECRPRFRELVSEFSRMARDPQRFVVJQNEDLGPASPLDSTFYRSLLEDDDWGDLVDA
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 NOPDVR POPPS PREGPL PAAR PAGATLERAKTLS PGKNGVVKDVFAFGGAVENPEYLTPQ
 The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by aliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat or prevent cancer in the may be used to the treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
 HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; cancer; prostate cancer; ovarian cancer; lung cancer;
 HER-2/neu extracellular domain/phosphorylation domain fusion useful for vaccinating against breast, ovarian, colon, lung a
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 AAB21198 standard; protein; 1255
 Claim 52; Fig 7; 128pp; English.
 28-JAN-2000; 2000WO-US02164
 99US-0117976
 (CORI-) CORIXA CORP.
(SMIK) SMITHKLINE BEECHAM.
 (first entry)
 Human HER-2/neu protein.
 Gheysen
 WPI; 2000-505976/45.
 N-PSDB; AAA89736.
 cancers
 WO200044899-A1
 29-JAN-1999;
 MA,
 colon cancer
 12-JAN-2001
 03-AUG-2000
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 EEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGDLTLGLEPSEEAPRSPLAPSEG
 The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
 cancer;
 an erbB 2 receptor protein designated SPLICE the protein are useful for treatment of cancer
 erbB-2 receptor protein; cell transformation disorder;
 tumor cell proliferation; tissue degeneration; arthropathy;
bone resorption; inflammatory disease; degenerative disorder;
wound healing.
 acid sequence of the SPLICE erbB-2 receptor protein.
 nervous system and wound healing
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 AAY84780 standard; Protein; 1255
 3; Fig 2; 60pp; English.
 99WO-CA00912
 98US-0165192
 entry)
 Siegel PM;
 acid encoding inhibitors of
 MCMASTER
 2000-303768/26.
 (first
 N-PSDB; AAA14812
 WO200020579-A1
 Bapiens
 01-OCT-1999;
 (UYMC-) UNIV
 02-OCT-1998;
 08-AUG-2000
 13-APR-2000
 Muller WJ,
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 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 LAALCRWGLLLALLPPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 ELIYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
 DPLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 ||||||
|PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSG1CELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPALQRASPLTSIVSAVVG
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVA I KVLRENTS PKANKE I LDEAYVMAGVGS P
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 IDSECRPRERELVSEFSRMARDPQREVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG
 Gaps
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 Length 1255,
 Indels
 11;
 DB 21;
 3; Mismatches
 Score 6730;
Pred. No. 0;
 98.8%;
98.9%;
Query Match 98.8
Best Local Similarity 98.9
Matches 1241; Conservative
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 EEYLVPQQFFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSBDPTVPLPSETDGYVAPLTCSPQPEYV 1140
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
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 720
 780
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 HQSDV#SYGVTV#ELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGL PREYVNARHCL PCH PECQ PQNGSVTCFG PEADQCVACAHYKD PPFCVARC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTSPKANKEI LDEAYVMAGVGSP
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 HOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 EEYLVPQQGFFCPDPAPGAGGWVHRRRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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 The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as pl85 or c-erbB2).
 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
 New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
 NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
 Antigen-presenting cell; immunogenic; immune response; HER-2/neu; oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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0
 98.8%; Score 6730; DB 22; Length 1255; llarity 98.9%; Pred. No. 0; Conservative 3; Mismatches 11; Indels 0;
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 Claim 2; Page 41-46; 49pp; English.
 standard; Protein; 1255
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 Cheever MA, Hand-Zimmermann
 19-JAN-2001; 2001WO-US01850
 21-JAN-2000; 2000US-0177545
 Human HER-2/neu protein.
 2001-476112/51.
 (CORI-) CORIXA CORP
 1255 AA;
 Best Local Similarity
Matches 1241; Conserv
 N-PSDB; AAH23392
 WO200153463-A2.
 Homo sapiens
 25-SEP-2001
 26-JUL-2001
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 Also described are: (1) a clonal systems prepared Hark/Then epitopes (1).

Also described are: (1) a clonal systems of an epitope (1), bound to a culture in vitro and binds to a complex of an epitope (1), bound to a culture in vitro and binds to a complex of an epitope (1), bound to a culture an epitope and the peptide is less than 50 contiguous amino acids that have 100% identity with a native peptide sequence of HER2/neu; (3) a waccine composition (II) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimulant activities, and can be used in vaccines. (I), (II) and inducting or evaluating an immune response for the prevention and trearment of cancer. (I) and (III) are useful for conjudition and trearment of cancer. (I) and (III) are useful for and immune response to a tumour-associated antiquen when incubated with a Tlymphocyte sample form a patient and detecting the presence of bound T lymphocyte to (I) or (II). Epitope cantigen when incubated with a Tlymphocyte to (I) or (II). Epitope conjuded to antigen may be avoided. Selected epitopes that may be present in whole antigens may be avoided. Selected epitopes that may be present confined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine convoides the ability to direct and focus an immune response to multiple cumour-associated molecules addressing the problem of tumour escape due to cumour variability and reducing the likelihood of tumour escape due to antigen loss. And88286 to AAG89121 represent mino acid sequences used in exemplification of the present invention.
NOPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
 inducing cancer -
 present invention describes isolated prepared HER2/neu epitopes (1)
 Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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 Celis
 An isolated prepared HER2/neu epitope useful in a vaccine for cellular immune responses for the prevention and treatment of
 Chesnut R,
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 Southwood
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 Disclosure; Page 15; 199pp; English.
 AAG88267 standard; Protein; 1255
 ٦,
 HER2/neu amino acid sequence
 11-DEC-2000; 2000WO-US33591
 99US-0458299
 Sidney
 (first entry)
 WPI; 2001-374995/39.
 Sette A,
 1255 AA;
 (EPIM-) EPIMMUNE
 WO200141787-A1.
 10-DEC-1999;
 Homo sapiens
 11-SEP-2001
 isolated
 14-JUN-2001
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 AAG88267;
 Fikes J,
Keogh E;
 Sequence
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DB 22; Length 1255

8%; Score 6730;

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 IDSECRPRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020
 EEYLVPQQGFPCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080
 240
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 999
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 VEBCRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHNNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 ILLWWLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYVMAGVGSP
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 HQSDVWSYGVTVWELMTFGAKPYDG1PAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 Gaps
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 11;
 Pred. No. 0; 3; Mismatches
 98.98;
Best Local Similarity 98.9
Matches 1241, Conservative
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1141 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 ILLVVVLGVVFGILIKRRQOKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
 DPLNNQY IKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LILIDINRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGCARCKGPLPTDCCHEQC
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 1QEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRSLGSGLALIHHNTHLCFVHTV
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMP1WKPPDEEGACQPCP1NCTHSCVDLDDKGCPAEQRASPLTS1VSAVVG
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 LVHRDLAARNVLVKSPNHVKI TDFGLARLLDI DETEYHADGGKVPI KWMALES I LRRRFT
 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 IDSECRPRPRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 EEYLVPQQFFCPDPAPGAGGWYHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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tumors
 The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGDLTLGLEPSEEEAPRSPLAPSEG
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 1255
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 1255
 Gaps
 Human; Her-2; epidermal growth factor receptor 2; infection; cancer;
hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
 Novel antisense oligonucleotide which modulates the expression
Epidermal Growth Factor receptor, Her2, is useful for treating
inflammation or to prevent infection in humans -
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 Length 1255;
 Indels
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 Query Match
98.8%; Score 6730; D
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1241; Conservative 3; Mismatches
 Example 13; Page 95-107; 116pp; English
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 standard; Protein; 1255
 12-SEP-2001; 2001WO-US28572
 15-SEP-2000; 2000US-0663834
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 (first
 Her-2 protein.
 WPI; 2002-471192/50.
N-PSDB; AAD38904.
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 (ISIS-) ISIS PHARM
 1255
 WO200222636-A1
 protein
 Homo sapiens
 CF,
 23-SEP-2002
 AAE24067;
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 1141
 AAE24067
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AACA AAE24067
AACA AAE24067
AACA AAE24067
AACA AAE24067
AACA AAE24
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Best Local Similarity 98.9%;
Matches 1241; Conservative
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 The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human cleukcoyte antique (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for human malignancies, for stimulating and/or expanding T cells specific for human malignancies, for inhibiting the development of cancer in a parient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to continue therefore a suitable library, and to direct expression of a central and parient host cells with complementary stretches of the central mappropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-
Human, Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
 1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
 Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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 Kalos
 Lodes MJ,
 present sequence is human Her-2/neu protein.
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 Disclosure; Page 114-117; 129pp; English
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 Location/Qualifiers
 AAE20479 standard; Protein; 1255
 Cheever MA,
 14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 14-AUG-2001; 2001WO-US41733
 (first entry)
 Human Her-2/neu protein
 Vedvick
 2002-280758/32.
 (CORI-) CORIXA CORP
 Hand-zimmermann S,
Mcneill PD, Vedvic
 1255 AA;
 N-PSDB; AAD32743
 WO200214503-A2
 Homo sapiens
 01-JUL-2002
 21-FEB-2002
 1141
 1201
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 AAE20479;
 Region
 WPI:
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Length 1255;

DB 23;

6730;

Score

98.88;

Query Match

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 IDSECRPRERELVSEFSRMARDPQREVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020
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 420
 420
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 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT 900
 900
 HOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 960
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 9
 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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 DPLNNQYIKANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYVMAGVGSP
 RKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 EEYLVPQQGFFCPDPAPGAGGMVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
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 EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080
 Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain.
 1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor intracellular (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, incleic acids encoding them, viral vectors, and vaccines
 NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
 Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
tyrosine kinase; receptor; c-erbB2; gene therapy.
 Human Her-2/neu oncogene-encoded p185 glycoprotein
 /note= "phosphorylation domain'
 CORIXA CORP. SMITHKLINE BEECHAM BIOLOGICALS.
 /note= "intracellular
990..1255
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 AAM51143 standard; Protein; 1255
 Claim 68; Fig 7; 141pp; English.
 03-AUG-2001; 2001WO-US24283
 03-AUG-2000; 2000US-0632507
 (first entry)
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 Gheysen D;
 2002-241743/29.
 N-PSDB; ABA92250.
 WO200212341-A2
 17-JUN-2002
 Homo sapiens
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 1 MELAALCRWGLLIALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
 DPLNNQY1KANSKFIGITELOLRSLTEILKGGVLIQRNPOLCYODTILWKD1FHKNNOLA
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS11SAVVG
 RKVKVLGSGAPGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
 Gaps
comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltapD fragment). In immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
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 DB 23; Length 1255;
 Indels
 order to inhibit the development of cancer in a patient
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 98.8%; Score 6730; Di
98.9%; Pred. No. 0;
ive 3; Mismatches
 Query Match
Best Local Similarity 98.9
Matches 1241; Conservative
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haematological malignancy in patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polymucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acure myelogenous leukaemia (ML), chronic myelogenous leukaemia (ML), chronic myelogenous leukaemia (CLL), in MDS, myelomas. Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
 DPLNNQY1KANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKD1FHKNNQLA
 LILIDINRSRACHPCSPMCKGSRCWGESSEDCQSLIRTVCAGGCARCKGPLPTDCCHEQC
 LT.LIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFACCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 RKVKVLGSGAFGTVYKGIWI PDGENVKI PVA I KVLRENTSPKANKE I LDEA YVMAGVGSP
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
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 invention relates to a method
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 NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
 960
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 Inhibiting haematological malignancy development by administering polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide encoding the polypeptide, or antigen presenting cells expressing the
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGDLTLGLEPSEEEAPRSPLAPSEG
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 CLL;
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
 Human; Her-2/neu; cytostatic; haematological malignancy; CML;
acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
 Hand-zimmermann
 Disclosure; Page 71-74; 74pp; English
 Hodgkin's lymphoma; T cell therapy
 Her-2/neu polypeptide
 14-AUG-2000; 2000US-0638280.
28-SEP-2000; 2000US-0675904.
 13-AUG-2001; 2001WO-US25408
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N-PSDB; ABK10730.
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 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 DPLNNQY I KANSKFIGITELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 LTLIDINRSRACHPCSPMCKGSRCWGESSEHCQSLTRTVCAGGCARCKGPLPTDCCHEQC
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 VEECRVLOGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 1255
 c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568). X in AAR39583 represents the location of a stop codon in AAQ46083.
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
 etc
 Length 1433
 C-erbB-2 tumour
covarian cancer
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 Ring
 single chain Fv polypeptide binding to C
gen - for imaging or treating breast or
 6687;
No. 0;
 Tumour antigen; c-erbB-2; glycoprotein
 Disclosure; pages 48-54; 87pp; English.
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 tumour antigen
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 Score
Pred.
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 standard; Protein; 1433
 CETUS ONCOLOGY CORP. CREATIVE BIOMOLECULES
 98.2%;
98.3%;
 92US-0831967
 93WO-US01055
 entry)
 LL, Huston JS,
 c-erbB-2
 WPI; 1993-272889/34.
N-PSDB; AAQ46083.
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 Query Match
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| 1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTGSPQPEYV 1140 | 1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140 | 1141 NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200 | 1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200 | 1201 GGAAPQPHPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255 | 1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255 |
|------------------------------------------------------------------------|------------------------------------------------------------------------|------------------------------------------------------------------------|------------------------------------------------------------------------|------------------------------------------------------------------|-------------------------------------------------------------------|
| 108                                                                    | 108                                                                    | 114                                                                    | 114                                                                    | 120                                                              | 120                                                               |
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Search completed: July 22, 2003, 08:40:28 Job time: 43.9774 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 22, 2003, 08:25:54; Search time 22.9062 Seconds (without alignments) 5267.077 Million cell updates/sec Run on:

SEQ4-149-163-12 6810 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| · m       | Description           | protein-tyrosine k | protein-tyrosine k | p-185 precursor - | epidermal growth f |        |        |        | >      | kinase-related tra | epidermal growth f | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | epidermal growth f | kinase-related tra | protein-tyrosine k | protein-tyrosine k | epidermal growth f | •∙⊢    |        | protein-tyrosine k |        |        |        | >      | protein-tyrosine k | insulin-like growt | insulin receptor p | receptor |
|-----------|-----------------------|--------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|----------|
| SUMMARIES |                       | _                  | _                  |                   |                    | _      | _      | _      | ۵.     | _                  | _                  | _                  |                    |                    |                    | _                  |                    | _                  |                    | _      |        |                    |        |        |        | _      |                    |                    |                    |          |
| SU        | ΩI                    | A24571             | TVRTNU             | 148161            | COHOE              | A53183 | TVCHLV | A47253 | S06142 | A36223             | JC4387             | TVFVLV             | TWYUH              | 835745             | GOPFE              | S00727             | B44776             | TVFVEB             | A36325             | E88257 | S70712 | 870713             | A45558 | A42032 | A27131 | S13807 | S13808             | T43220             | INHUR              | A34157   |
|           | DB                    | ٦                  | -                  | ~                 | -4                 | ~      | -      | 7      | -      | ~                  | ~                  | ч                  | -                  | ~                  | -                  | ~                  | ~                  | -                  | ~                  | 7      | ~      | ~                  | -      | 7      | ~      | ~      | ~                  | 7                  | 1                  | 7        |
|           | Query<br>Match Length | 1255               | 26                 | 1254              | 21                 | 1210   | 1223   | 1308   | 1166   | 1342               | 1339               | 698                | 604                | 544                | 1330               | 545                | 540                | 540                | 644                | 1323   | 1374   | 1369               | 1717   | 527    | 843    | 346    | 311                | 1363               | 1382               | 37       |
| عن        | Query                 |                    | 87.2               | 87.1              | 46.4               | 46.0   | 45.7   | 43.7   |        | 35.6               | 34.4               | 25.9               | 25.0               | 24.2               | 24.2               | 4.                 | 23.8               | 23.8               | 3                  | 19.0   | 19.0   | 17.7               | 7      |        | •      |        | •                  |                    | 10.5               | 10.4     |
|           | Score                 | 6734               | 5935               | 5931.5            | 3160               | 3135   | 3109.5 | 2975.5 | 2684   | 2423.5             | 2339.5             | 1766.5             | 1703               | 1647               | 1645.5             | 1640               | 1623               | 1621               | 1530               | 1297   | 1297   | 1208               | 1162   | 1141   | 990.5  | 806.5  | 754.5              | 725                | 713                | 705.5    |
|           | Result<br>No.         | н                  | N                  | m                 | 4                  | Ŋ      | v      | 7      | æ      | Φ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19     | 20     | 21                 | 22     | 23     | 24     | 25     | 56                 | 27                 | 28                 | 29       |

| insulin receptor p<br>insulin-like growt | insulin receptor-r | protein-tyrosine k<br>insulin-like growe | ingulin-like growt | insulin receptor -<br>insulin receptor - | insulin receptor ( | protein-tyrosine k | tyrosine kinase Mp | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k |
|------------------------------------------|--------------------|------------------------------------------|--------------------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A36080<br>T43212                         | A36502<br>B36502   | T18534<br>IGHUR1                         | A33837             | T30346<br>A56081                         | S57245             | A54092             | S49004             | 805582             | S33596             | A36355             |
| ~ ~                                      | 00                 | 7 -                                      | 0                  | 7 7                                      | 04 C               | 9 (7               | 7                  | -                  | ~                  | 7                  |
| 1383                                     | 1300               | 1477                                     | 1371               | 1390                                     | 2101               | 987                | 977                | 1114               | 1091               | 916                |
| 10.4                                     | 10.3               | 0 0<br>0 0                               | 4.0                | 9 9<br>9 . 1                             | 0 a                | 8.7                | 8.7                | 9.8                | 8.6                | 9.8                |
| 705                                      | 698.5<br>684       | 669                                      | 639                | 618.5                                    | 615                | 591                | 589.5              | 288                | 586                | 584.5              |
| 30                                       | 33                 | 34                                       | 36                 | 38                                       | 39                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

|   | RESULT 1<br>A24571                                                                                                                                                                       |
|---|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|   | protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human<br>N.Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein e<br>C.Snecias: Huma sanians (man) |
|   |                                                                                                                                                                                          |
|   | K;Yamamoto, T.; Itawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T<br>Nature 319, 230-234, 1986                                                                       |
|   | A;ittle: Similarity of procein encoded by the human c-erb-B-2 gene to epidermal growt<br>A;Reference number: A24571; MUID:86118663; PMID:3003577                                         |
|   | A;Arcebsion: A243/1<br>A;Molecule type: mRNA<br>A;Residues: 1-1255                                                                                                                       |
|   | A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198<br>R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.                                                           |
|   | Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985 A:Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epid                                                  |
|   | A; Accession: A25491; MUID: 86016729; PMID: 2995967 A; Accession: A25491                                                                                                                 |
|   | A;MOLECULE Lype: DNA<br>A;Residues: 737-1031 <sem></sem>                                                                                                                                 |
|   | PID:9553282                                                                                                                                                                              |
|   | к;соцьвелв, L.; Yang-Féng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.: Seeburg<br>Science 230, 1132-1139, 1985                                                                    |
|   | A:Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chro                                                                                                    |
| _ | A;Accession: A44188                                                                                                                                                                      |
|   | A; Molecule type: DNA                                                                                                                                                                    |
|   | A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989                                                                                                                 |
|   | A; Accession: B44188<br>A: Molecule type: mRNa                                                                                                                                           |
|   | A;Residues: 1-517, MALL, 522, S', 524-654, V', 656-1169, A', 1171-1255 <cou2></cou2>                                                                                                     |
|   | A;Cross-references: GB:M11730; NID:g183986<br>R:King C R : Krang M H : Aarongen S A                                                                                                      |
|   | Science 229, 974-976, 1985                                                                                                                                                               |
|   | A/IILLe: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.<br>A/Reference number: IS9509; MUID:85272597; PMID:2992089                                           |
|   | A;Accession: 159509                                                                                                                                                                      |
| _ | A Molecule type: DNA                                                                                                                                                                     |
|   | A;KBBIQUEB: BJZ-2909 KERZy><br>A:Gross-references: GR-1,2039c, NID-nasosno, ordn.,2025cono 1. ord.,2050co                                                                                |
|   | R.Tal. M. King, C.R., Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D. Mol. Cell Riol 7 2507-261                                                                                    |
|   | A,Title: Human HER2 (new) promoter: evidence for multiple mechanisms for transcriptio A.Reference number: 157620. MITD, 87386898. DATE, 303058                                           |
|   | A, Accession: 157622                                                                                                                                                                     |
|   | A;Status: translated from GB/EMBL/DDBJ<br>A;Molecule type: DNA                                                                                                                           |
| _ | A;Residues: 1-191 <tal></tal>                                                                                                                                                            |

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R. Hargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A.Fitle: The neu oncogene encodes an epidermal growth factor receptor-related protein A.Fitle: The neu oncogene encodes an epidermal growth factor receptor-related protein A.Fiteference number: A24562; MUID:86118662; PMID:3945311
A.Accession: A24562
A.Molecule type: mRNA
A.Residues: 1-1260 cBAR>
A.Residues: 1-1260 cBAR>
A.Residues: 1-1260 cBAR>
A.Residues: 1-1260 LBAR>
A.Residues: 1-1260 LBAR>
A.Cross-references: EMBL:X03362; NID:956745; PIDN:CAA27059.1; PID:956746
B.Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohe Carcinogenesis 12, 1975-1979, 1991
A.Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals for thiazolyl] formamide or N-methyl-N-nitrosourea.
A.Reference number: A61204; MUID:92035293; PMID:1682063
 C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phos F;1-19/Domain: signal sequence #status predicted <SIG. F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
 C.Species: Rattus norvegicus (Norway rat)
C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
C.Accession: A24562; A61204
 1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEVV
 PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS11SAVVG
 781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 LVHRDLAARNVLVKSPNHVKITDFCLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
 901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 HQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1DVYM1MVKCWM
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
 1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
 Val
 aB
 protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
 52
 A;Molecule type: DNA
A;Residues: 637-663,'V',665-702 <MAS>
A;Note: authors translated the codon GCA for residue
 A;Status: preliminary
 A; Accession: A61204
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Fil-12/Domain: Signal sequence #status predicted <SIG>Fil-21/Domain: Signal sequence #status predicted <SIG>Fil-21/Domain: extracellular #status predicted <EXT>Fil-22-1255/Product: procein-tyrosine kinase erbB2 #status predicted <EXT>Fil-304/Domain: extracellular #status predicted <EXT>Fil-304/Domain: EGF receptor extracellular domain repeat <EE2>Fil-305-605/Domain: EGF receptor extracellular domain repeat <EE2>Fil-305-605/Domain: EGF receptor extracellular domain repeat <EE2>Fil-305-605/Domain: protein #status predicted <IVMN-Fil-305-605/Domain: intracellular #status predicted <IVNT>Fil-305-700-71,629/Binding site: carbohydrate (Asn) (covalent) #status predicted Fil-305-71,629/Binding site: carbohydrate (Asn) (covalent) #status predicted Fil-305-71,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 3d
 A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C; Superfamily: epidermal growth factor receptor; protein kinase homology C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
 ö
 ELTYLPTNASLSFLQDIQEVQCYVLIAHNOVROVPLORLRIVRGTOLFEDNYALAVLDNG 120
 IGITELNKSRACHPCSPMCKGSKCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540
 9
 AGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
 VYYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
 420
 480
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480
 9
 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 PSGVKPDLSYMPIWKPPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
 Gaps
 ö
 Length 1255;
 10; Indels
 98.9%; Score 6734; DB 1; 98.8%; Pred. No. 7.4e-268; iive 5; Mismatches 10;
 A,Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Map position: 17421.1-17421.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
 Best Local Similarity 98.8
Matches 1240; Conservative
 Similarity
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1918 precursor - golden hamster
C; Species: Mesocricetus auratus (golden hamster)
C; Species: Mesocricetus auratus (golden hamster)
C; Date: 0.2-011-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C; Jaccession: 148161
R; Nakamura, T; Ushijima, T; Ishizaka, Y; Nagao, M; Arai, M; Yamazaki, Y; I Gene 140, 251-255, 1994
A; Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A; Accession: 148161
A; Cross-references: GB: D16295; NID: 9493236; PIDN: BAA03801.1; PID: 9747595
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: Applomain: protein kinase homology < KIN>
E; 726-734/Region: protein kinase ATP-binding motif
 YVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLT 1198
 1144 YVNQSEVQPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLV 1203
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
 EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPE
 1 MELAAWCGWGLLLALLSPGASGTQVCTGTDMKLRLPASPETHLDIVRHLYQGCQVVQGNL
 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKF
 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
 DAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPS
 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 181 IGITELNRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGCARCKGPLPTDCCHEOC
 1;
 2; Length 1254;
 104; Indels
 87.1%; Score 5931.5; DB 2;
86.9%; Pred. No. 4.2e-235;
tive 59; Mismatches 104;
 Query Match
Best Local Similarity 86.9°
Matches 1091; Conservative
 1084
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 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
 DPLNNTTPVT-GASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSK 179
 663
 723
 PTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC 958
 63
 #status
 F;658-680/Domain: transmembrane #status predicted <TWN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #statu
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted
 244 CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMHNPEGRYTFGASCVTTC
 VPWDQLFRNPHQALLHTANRPEDE-CVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGO
 FIGITELNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQ
 CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
 PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSA
 PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
 424 RDLSVFQNLRIIRGRILHDGAYSLTLQGLGIHSLGLRSLRELGSGLALIHRNAHLCFVHT
 ECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVA
 RCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAV
 RCPSGVKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASPVTFIIATV
 ELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTSPKANKEI LDEAYVMAGVG
 SPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLED
 SPYVSRLIGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNMCVQ1AKGMSYLED
 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 NIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLOVFETLEEITGYLYISAWPDSL
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 Gaps
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 Indels
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87.1%; Pred. No. 3e-235;
Live 51; Mismatches 109;
 Query Match
Best Local Similarity 87.1%
Matches 1095; Conservative
 360
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 124
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A)Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A)Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
A;Note: the authors translated the codon AAG for residue 540 as Asn
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the human epidermal A;Accession: A2572; MUID:85270438; PMID:2931899
A;Reference number: A25772; MUID:85270438; PMID:2931899
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-29 < ISBA
A;Cross-references: GB:MI1234; NID:g181981; PIDN:AAA52370.1; PID:g553272
A;Residues: 1-29 < ISBA
A;Cross-references: GB:MI1234; NID:g181981; PIDN:AAA52370.1; PID:g553272
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identificatio:
A;Reference number: S30024; MUID:88217333; PMID:3329716
 Air Reference number: 530024; MUID:8821733; PMID:3329716

Air Reference number: 530024; MUID:8821733; PMID:3329716

Air Residues: 1-29 - 4R2>

Air Coss -references: EMBL.X06370; NID:9313118; PIDN:CAA29668.1; PID:9313119

Air Relator, J. D.; Waterfield, M.D.

J. Biol. Chem. 266, 1746-1753, 1991

Air Residues: 1-29 - 4RJA

Air Coss -references: GMR 18425; MUID:93100767; PMID:398448

Air Coss -references: GMR 18425; MUID:931007677; PMID:398448

Air Coss -references: GMR 18425; MUID:931007677; PMID:398448

Air Coss -references: GMR 18425; MUID:9310977; PIDN:AA63171.1; PID:9553271

Air Coss -references: GMR 18425; MUID:9318377; PIDN:AA63171.1; PID:9553271

Air Coss -references: GMR 18425; MUID:9318377; PIDN:AA63171.1; PID:9553271

Air Coss -references: And 18426; MUID:9318377; PIDN:AA63171.1; PID:9553271

Air Coss -references: And 18426; MUID:9318377; PIDN:AA63171.1; PID:9553271

Air Coss -references: And 18426; MUID:931839; PMID:6330563

Air Lie: Human epiderance and 18426; MUID:931829; PMID:6330563

Air Coss -references: And 18426; MUID:93182; PMID:6330563

Air Coss -references: And 18426; MUID:9418372; PMID:6326261

Air Coss -references: And 18426; MUID:94196372; PMID:6324343

Air Reference number: Adoct MUID: Air Coss - Air Muid: Air MUID:941963780

Air Reference number: Adoct MUID:94196372; PMID:6324343

Air Reference number: Adoct MUID:941963780

Air Reference number: Adoct MUID:9419637
 A/Accession: A60143
A/Molecule type: protein
A/Rosadues: 740-744, XX, 746-747 <RUS>
B/Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A/Fitle: ATP-stimulated interaction between epidermal growth factor receptor and
A/Fitle: Malous A/Forestion; receptor activity
 PMID: 6328312
Reference number: A00641; MUID:84219729;
 A;Accession: A00641
A;Molecule type: mRNA
A;Residues: 1-1210 <ULL>
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 rg, P.H.
Nature 309, 418-425, 1984
A,Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression
 epidermal growth factor receptor precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Specias: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999
C;Accession: A00641; A25772; $30024; A38672; A00642; A43615; A23062; A05281; A60143;
R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.
 961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPSSPLDSTFYRSLLEDDDMGDLVDA 1020
 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140
 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
 1141 NQPEVRPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFTFGGAVENPEYLVPR 1200
 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020
 840
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 361 IQEFAGCKKIFGSLAFLPESFDGNPSSGIAPLTPEQLQVFETLEEITGYLYISAMPDSLH 420
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 540
 PWDQLFRNPHQALLHSGNPSEEECGLKDFACYPLCAHGHCWGPGPTQCVNCSHFLRGQEC 540
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 720
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 960
 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
 EEYLVPQQGFFFPDPAPGAGSTAHRRHRSSSTRSGGGELTLGMEPSGEEPPRSPLAPSEG
 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
 PSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
 PSGVKPDLSYMPIWKYPDEEGMCQPCPINCTHSCVDLDERGCPAEQRASPATSIIATVVG
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 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWIALESILRRRFT
 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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Cypecies: Mus musculus (house mouse)
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Cypecession: AS3183; A49818; S24942; A28941; S45325; I49643
Cypecession: AS3183; A49818; S24942; A28941; S45325; I49643
Ribuetteke, N.C.; Philips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A Genes Dev. 8, 399-413, 1994
A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF recepto A;Reference number: A53183; MUID:94170986; PMID:8125255
A;Accession: A53183
A;Accession: A53818

 1014 DEYLIPQOGFF-----SSPSTSRTPLLSSLS 1039
 1021 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
 |:|| | :| | :| | :| | 1111|
1092 YINQ-SVPKRPAGSVQNPVYHNQPLNP-----APSRDPHYQD--PHSTAVGNPEYLN
 MGENNTL-VWKYADAGHVCHLCHPNCTYGCTGPGLEGCPTNGPKIP--SIATGMVGALLL
 LLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELR
 KVKVLGSGAFGTVYKG1W1PDGENVK1PVA1KVLRENTSPKANKE1LDEAYVMAGVGSPY
 VSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRL
 VHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTH
 1198 TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----DP-----PERGAPPSTFKGTP
 DSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDA
 1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET---DGYVAPLTCSPQPE
 1141 TVQ-----PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGS-
 QSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMI
 1139 YVNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-
 epidermal growth factor receptor precursor - mouse
 TAENPEYL 1249
 1191 TAENAEYL 1198
 A;Reference number: S24942
A;Accession: S24942
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 A;Cross-references: GDB:120610; OMIM:131550
A;Map position: 7p12.3-7p12.1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; protein: Bignal sequence #status predicted <BGG>
F;25-110/Product: EGF receptor #status predicted <EGT>
F;35-100/Domain: EGF receptor extracellular domain repeat <EED>
F;30-600/Domain: EGF receptor extracellular domain repeat <EED>
F;30-600/Domain: transmembrane #status predicted <TMM>
F;66-660/Domain: intracellular #status predicted <TMM>
F;710-975/Domain: protein kinase homology <KIN>
F;710-975/Domain: protein kinase ATP-binding motification: protein kinase ATP-binding ATP-binding ATP-binding ATP-binding ATP-binding ATP-bindi
 O.J.
 (covalent) #status predio
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J Cell 59, 33-43, 1989
A;Title: Functional independence of the epidermal growth factor receptor from a domain A;Reference number: A33331; MUID:90003233; PMID:2790960
A;Contents: annotation; internalization signal C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor
 23,
 |: ||:|| :| |: || || || || || ::| |:| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
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 TGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYL 304
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 FONLOVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQ 484
 KPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG---I 661
 73
 68
 ONHLGSCQKCDPSCPNGSCWGAGGENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGC
 AGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSV
 11 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
 69 ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
 74 YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNMYYENSYALAVLSNYD-----
 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKFIGITEL--
 -NRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGC
 STDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEF
 LFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEEC
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 Query Match
46.4%; Score 3160; DB 1; Length 1210;
Best Local Similarity 49.8%; Pred. No. 5.4e-122;
Matches 631; Conservative 177; Mismatches 348; Indels 112;
 F;999-1046/Rēgion: coated-pit mediated internalization signal
F;1047-1210/Region: inhibitory
F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn)
F;745/Active site: Lys #status experimental
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 A; Gene: GDB: EGFR
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 TPNQKTKIMMNRAEKDCKAVNHVCNPLCSSEGGWGPEPRDCVSCQNVSRGRECVEKCNIL
 PRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEBYLV
 SVPKRPAGSVQNPVYHNQPLHP-----APGRDLHYQN--PHSNAVGNPEYLNTAQ--
 SYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECR
 1021 PQQGFF-----SRTPLLSSLSATSN-
 NPHOALLHTANRPEDECVGEGLACHOLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVL
 QGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPD
 LSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVL
 GVVFGI - LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVL
 GICLISTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDL
 AARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVW
 SYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPOPPICTIDVYMIMVKCWMIDADSR
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 1144 DVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TPQGG
 AAPQPHPPPAFSPAFDNLYYWDQ-----DP----PERGAPPSTFKGTPTAENP
 epidernal growth factor receptor precursor - chicken
N;Concains: protein-tyrosine kinase (BC 2.7.1.112) erbB
C;Species: Gallus gallus (chicken)
C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-C;Accession: A27720; A00643
R;Lax, I; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ull
Mol. Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidernal growth factor (EGF) receptor: CDNA cloning,
A;Reference number: A27720; MUID:88261272; PMID:3260329
 1247 EYLGLDVP 1254
 EYLRVAPP 1203
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A; Molecule type: mRNA
A; Residues: 969-971, 'K', 973-1115,'D' <EIS>
A; Cross-references: EMBL:212608
R; Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A; Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in A; Reference number: A28941; MUID:88330814; PMID:3138233
A; Accession: A28941
A; Molecule type: protein
A; Residues: 689-694, 'X', 696-704,'L',706-707; 989-992,'XX', 995-996,'X', 998-1000; 1002-1009, R; Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
R; Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
R; Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
R; Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
A; Reference number: S45325
A; Reference number: S45325
A; Reterence number: S45325
A; Reterence number: S45325
A; Reterence number: BMBL:X78987; NID:9488830; PIDN:CAA55587.1; PID:9488831
B; Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
A; Cross-references: EMBL:X78987; NID:9488830; PIDN:CAA55587.1; PID:9488831
B; Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
A; Title: Expression of the epidermal growth factor receptor gene is regulated in mouse be A; Reference number: 149643; MUID:93126380; PMID:7678348
 A, Status: translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Genetics:
A, Genetics
 124
 247
 243
 307
 ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
 VGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGC 367
 73
 SCHOOL SC
 KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD
 74 YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN-----
 LLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKFIGITELNR
 KKI FGSLAFLPES FDGDPASNTAPLQPEQLQVFETLEETTGYLYISAWPDSLPDLSVFQN
 SRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGP
 Gaps
 Ouery Match 46.0%; Score 3135; DB 2; Length 1210; Best Local Similarity 49.6%; Pred. No. 5.7e-121; Matches 629; Conservative 171; Mismatches 366; Indels 102;
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 pecific protein kinase
F.1-30/Domain: signal sequence #status predicted <SIG>F.1-122/Product: epidemal growth factor receptor #status predicted <MAT>
F.31-122/Product: epidemal growth factor receptor #status predicted <EXT>
F.31-654/Domain: extracellular #status predicted <EXT>
F.31-654/Domain: EGF receptor extracellular domain repeat <EEI>F.397-610/Domain: EGF receptor extracellular domain repeat <EE2>
F.55-677/Domain: DFF receptor extracellular domain repeat <EE2>
F.55-677/Domain: protein kinase homology <KIN>
F.79-984/Domain: intracellular #status predicted <INT>
F.79-984/Domain: protein kinase homology <KIN>
F.79-984/Domain: protein kinase ATP-binding motif
F.72-735/Region: protein kinase ATP-binding site: carbohydrate (Thr) (covalent) #status predicted
F.7192-650/Binding site: carbohydrate (Ser) (covalent) (by protein kinase C) #status predicted
F.754/Active site: Lys #status predicted
F.7100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat
 A,Gene: erbB
C,Superfamily: epidermal growth factor receptor; protein kinase homology
C,Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
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A;Accession: A27720
A;Molecule type: mRNA
A;Residues: 1-1223 <LLAX>
A;Cross-references: GB:M20386
A;Cross-references: GB:M20386
Call 41, 719-726, 1985
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pi
A;Reference number: A00643; MUID:8522822; PMID:2988784
 121
 181
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 302
 PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSA 359
 361
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 PDLSVFQNLQVIRGRILHNGAYSLTLOGLGISWLGLRSLRSLGSGLALIHHNTHLCFVHT 479
 481
 541
 540 CVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAHYKDPPFC 596
 61
 72
 122 PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKFI
 CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
 NIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL
 RWGLLLALLPPGAA----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
 LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD
 182 GITEL-NRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGCA-RCKGPLPTDCCHEQ
 480 VPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQE
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45.7%; Score 3109.5; DB 1; Length 1223;
Best Local Similarity 48.6%; Pred. No. 6.3e-120;
Matches 630; Conservative 175; Mismatches 347; Indels 145; Gaps
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 A; Molecule type: mRNA
A; Residues: $85-1223 <NIL>
A; Crose-references: GB:M10066
C; Genetics:
 A; Accession: A00643
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Cispecies: Homo sapiens (man)
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Cispecies: Us.a., av. Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.;
Riplowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.;
Riplowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.;
A; Reference number: A47253
A; Reference number: A47253
A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Residues: 1-1308 exp.o.
A; Residues: 1-1308 exp.o.
A; Note: sequence extracted from NCBI backbone (NCBIP:126842)
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor
F; 716-981/Domain: protein kinase homology <KIN>
F; 724-732/Region: protein kinase ATP-binding motif 1014 1074 1127 1094 1126 AISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLAKTVFESSPYWIQSGNHQIN 1177 L-----PAPEYVNQ--LMPKKPS------TAMVQNQIYNNISLT 1125 959 715 716 775 835 601 657 176 836 895 896 955 926 597 VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS VKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDM 776 GVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSY LEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIL 1015 GDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP -----AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----657 AVV-GILLVVVLGVVFGILIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRIL KETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMA 1075 L----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGY 1128 VAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVF--LDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP 1214 -DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1254

Tue Jul

| 43.7%; Score 2975.5; DB 2; Length 1308;<br>nilarity 45.2%; Pred. No. 2e-114;<br>Conservative 185; Mismatches 379; Indels 173; Gaps 28; | MGLILALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTY 64 | MVSLĽVAAGTVQPSDSQSVČAGTENKĽSSLSDLEQQYRALRKYYENČEVVMGNLEITS 67 | LPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN 124 |   |            | ELNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG 243 | NGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPYVSDCCHRECAGG 237 | 0   | 5   | LSTIVOGSCTLVCPLHNQEVTAEDGTORCEKCSKPCARVCYGLGMEHLREVRAVTSANIQE 363 | 42  |     | VFQNLQVIRGRILHNGAVSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD 483 | SNLVTIGGRVLYSGLSLLILKQQGITSLQFQSLKEISAGNIYITDNSNLCYYHTINWT 475 | OLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGGECVEE 543 | 9   | 0   | GVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPL 651 | I<br>YYPWTGHSTLE | VSAVV | 2,  | -        :: | VWAGVGSPYVSRLLGICLTSTVOLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA 830 | ALIMASMDHPPHLVRLLGGVCLSPTIQLVTQLMPHGCLLEYVHEHKDNIGSQLLLNWCVQIA 828 | KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA 890 | MMYLEERRIVHRDIAARNVIVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPIKMA 888 | SILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID | SCIHYRKFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPICTID 948 | VYMIMVKGWMIDSECRPRFRELVSEFSRWARDPORFVVIONED-LGPASPLDSTFYRSLL 1009    -   -        - |   |
|----------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|---------------------------------------------------------------|------------------------------------------------------------------|---|------------|------------------------------------------------------------------|----------------------------------------------------------------|-----|-----|-------------------------------------------------------------------|-----|-----|------------------------------------------------------------------|----------------------------------------------------------------|------------------------------------------------------------------|-----|-----|-------------------------------------------------------|------------------|-------|-----|-------------|----------------------------------------------------------------|--------------------------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------------|------------------------------------------------------------|-----------------------------------------------------------------|-------------------------------------------------------------------------------------|---|
| Simil<br>9, C                                                                                                                          |                                                             |                                                               |                                                                  |   | — <u>x</u> |                                                                  |                                                                |     |     |                                                                   |     | — ш |                                                                  |                                                                |                                                                  |     |     |                                                       |                  | TS    |     |             |                                                                |                                                                    |                                                                  |                                                               | 3=                                                         | H<br>H                                                          |                                                                                     |   |
| Query Match<br>Best Local S<br>Matches 609                                                                                             | 6                                                           | 60                                                            | 68                                                               |   | 128        | 185                                                              | 179                                                            | 4   | 238 | 304                                                               | ف ، | 356 | 424                                                              | 416                                                            | 484                                                              | 544 | 536 | 603                                                   | 965              | 652   | 711 | 709         | 171                                                            | 169                                                                | 831                                                              | 829                                                           | 68                                                         | <b>x</b> 0                                                      | . 951                                                                               |   |
| J m 2                                                                                                                                  | δ                                                           | qq                                                            | è 8                                                              | ò | qq         | ò                                                                | g                                                              | ð : | 8 ( | <u></u> 8                                                         | ò   | qq  | ò                                                                | qq                                                             | <u>ک</u> ۾                                                       | ò   | . d | ò                                                     | 셤                | ò 5   | 8 8 | 6           | ò                                                              | QQ                                                                 | δ                                                                | පු                                                            | ò :                                                        | g                                                               | £ 5                                                                                 | δ |

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A;Map position: Y
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
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F;1-25/Domain: signal sequence #status predicted <81G>
F;2-1166/Product: kinase-related transforming protein (Tu) #status predicted <MAT>
F;70-972/Domain: protein kinase homology <KIN>
F;715-723/Region: protein kinase ATP-binding motif
 protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish
N;Alternate names: epidermal growth factor receptor homolog; kinase-related transform
C;Specias: Xiphophorus maculatus (southern platyfish)
C;Accession: Sofi42; S13809
R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, A.; Robe
Nature 341, 415-421, 1989
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu
A;Reference number: Sofi42; MUD: 90015140; PMID: 2797166
 A; Molecule type: DNA
A; Residues: 1-1166 <WIT>
A; Residues: 1-1166 <WIT>
A; Cross-references: BEBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291
A; Crossene 6, 73-80, 1991
A; Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphopl A; Ricle: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphopl A; Reference number: 813807; MUID:91125882; PMID:1846957
A; Accession: S13809
A; Status: preliminary; translation not shown
A; Molecule type: DNA
 1212
-----PLAP-SEGAGSDVFDGDLGMGAAKGLQS 1100
 101 LPTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPR 1153
 1213 ------PPSTF 1237
 1200 DEYVNEPLYLNTFANTLGKAEYLKONILSMPEKAKKAFDNPDYWNHSLPPRSTLQHPDYL 1259
 28;
 60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119
 120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSK 179
 59
 62
 8 AALLQ--LLLVLSISRCCSTDPDRKVCQGTSNQMTM---LDNHYLKMKKMYSGCNVVLEN
 1154 EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPA-
 Query Match
39.4%; Score 2684; DB 1; Length 1166;
Best Local Similarity 45.2%; Pred. No. 1.4e-102;
Matches 573; Conservative 165; Mismatches 391; Indels 138; Gaps
 4 AALCRWGLLLALLPPGAAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
 A;Residues: 821-1025,'N',1027-1098,'A',1100-1166 <ADA>
A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
 1238 KGTPT-----1249
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1342 <KRA>
A;Residues: 1-1342 <KRA>
A;Residues: 1-1342 <KRA>
B;Residues: 1-1342 <KRA>
A;Residues: 1-1342 <KRA>
A;Residues: 1-1342 <KRA>
A;References: GB:M29366
B;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
A;Title: Molecular cloning and expression of another epidermal growth factor receptor A;Reference number: 159164; MUID:90311312; PMID:2164210
 the ERBB/epiderma
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 A.Residues: 1-559, "G', 561-957,'F', 959-1063, 'G',1065-1342 <RES>
A.Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
CGenetics:
A.Genetics: GDB:ERBB3; HER3
A.Cross-references: GDB:119880; OMIM:190151
A.Rep position: 12q13-12q13
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C.Skeywords: ATP; phosphotransferase
F;707-972/Domain: protein kinase homology <KIN>
F;715-723/Region: protein kinase ATP-binding motif
 32,
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 127
 187
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 ---NSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRAE---IVVKD 178
 237
 247 PKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST 306
 67
 DVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAG 366
 CKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQ 426
 485
 70
 C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
 11 GLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGH
 kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human
 10 GLLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT
 68 NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT
 71 NADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVM-----LNYNT
 128 PVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKFIGITELN
 188 RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG
 NLQVIRGRILHNGAYS-LTLQGLGISMLGLRSIRBLGSGLALIHHNTHLCFVHTVPWDQL
 Gaps
 Query Match 35.6%; Score 2423.5; DB 2; Length 1342; Best Local Similarity 40.7%; Pred. No. 6.9e-92; Matches 533; Conservative 191; Mismatches 458; Indels 129;
 R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A. Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A;Title: Isolation and characterization of ERBB3, a third member of A;Reference number: A36223; MUID:90083234; PMID:2687875
 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-559,'G'.561-947 'P' orn
 C; Accession: A36223; I59164
1244 ENPEYLG 1250
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 A; Accession: A36223
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 polysoment growth factor receptor homolog precursor - rat

Willternate names: ErbB3 protein; HER3 protein
Cispecies: Rattues norvegicus (Norway rat)
Cispecies: Rattues norvegicus (Norway rat)
Cibate: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
Circession: JC4387 # H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
Gene 165, 279-284, 1995
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.
A;Reference number: JC4387; MUID:96096535; PMID:8522190
A;Recession: JC4387
A;Molecule Cype: mRNA
A;Residues: 1-1339 <-HEL>
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NLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSLNWTKV 473
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 605 KPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRA----SPLTSIVSAVVG
 661 ILLVVVLGVVFGILIKRROQKIR-KYTMRRLLQETELVEPLTPSGAMPNOAOMRILKETE
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 MIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPA---SPLDSTFYRSLLEDDDMGD
 949 MIDENIRPTEKELANEFTRMARDPPRYLVIKRES-GPGIAPGPEPHGLTNKKLEEVELEP
 1017 LVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGDLTLGLEP-SEEEAPRSPL
 1008 ELDLDLDLEAEED--------NEATTLGSALSLPVGTLNRPRGSQSLL
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 RPSSLEELGYEYMDVGSDLSASLGSTOSCPLHPVPIMPTAGTTPDEDYEYM 1263
 --PLTCSPQPE----YVNQPDVRPQPPSPREGP-
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 A.Experimental source: liver
A.Experimental source: liver
A.Note: The authors translated the codon AAC for residue 369 as int and A.Note: The authors translated the codon AAC for residue 369 as int and A.Note: This protein is a functional heregulin receptor that transduces (C.Genetics: A.Gene: ErbB3
A.Gene: ErbB3
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein C.Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembra F;1-19/Domain: signal sequence #status predicted <AIG>F:20-1339/Product: epidermal growth factor homolog #status predicted <MAT>F:640-659/Domain: transmembrane #status predicted <TWM>F:705-970/Domain: protein kinase homology <KIN>F:713-721/Region: protein kinase ATP-binding motif F:939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosp
 LELTYLPTNASLSFLQDIQEVQCYVLIAHNQVRQVPLQRLRIVRCTQLFEDNYALAVLDN
 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA
 SNIDGFVNCTKILGNLDFLITGLNVDPWHKIPALDPEKLNVFRTVREITGYLNIQSWPPH
 180 FIGITELNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE
 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTS
 ANIQEPAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYI SAWPDS
 LPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFV
 HTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR
 QQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFC
 597 VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSC---VDLDDKGCPAEQRASPLTSI
 586 VNSCPHGILG--AKGPIXKYPDAQNECRPCHENCTOGCNGPELQDCLGQAEVLMSKPHLV
 LAALCRWGLLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
 LOVI.C----FILSLARGSEMGNSQAVCPGTLNGLSVTGDADNQYQTLYKLYEKCEVVMGN
 655 VSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMR
 Gaps
 Indels 155;
Cross-references: GB:U29339; NID:g915389; PID:g915390
Experimental source: liver
Note: The authors translated the codon AAC for residue 369 as
 Query Match
34.4%; Score 2339.5; DB 2;
Best Local Similarity 40.8%; Pred. No. 1.9e-88;
Matches 523; Conservative 172; Mismatches 433; Ii
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| Db 117 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 172  Qy 697 VEPLTPSGAMPNQAQMRILKETELRKVKVLLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR 756    | Db 233 EATSPRANKEILDEAYVMASVDRPHVCRLIGICLTSTYQLITGLMPYGCLLDYIREHKDN 292  Qy 817 LGSQDLLNWCMQIAKGMYSYLEDVRLYHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE 876    1 | Qy   877 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE 936<br>          | QY         937 KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG         995           DD         413 KGERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLVIQGDERMH         472 | QY         996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSG 1055 | QY 1056 GGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110  Db 514SRTPLLSSLSATSNNSATNCIDRNGQGHPVREDSFVQ 550           | QY                                                                    | QY         1169 RAKTLSPGKNGVVKDVF                                                                                                                                                                                                                                                                                                                                                                           | pro                   | A,Title: The erbB gene of avian erythroblastosis virus is a member of the src gene fan A,Reference number: A00644; MUID:84026539; PMID:631329 A,Rocession: A00644 A,Molecule type: DNA A,Residues: 1-604 < YAM> A,Residues: 1-604 < YAMA A,Residues: 1 | A;Molecule type: DNA A;Residues: 1-28, W',30-139,'F',141-145,'V',147-152 <deb> A;Cross-references: GB:K02006 C;Genetics: A;Gene: erbB C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferaes; transforming protein; tyrosine-spe F;130-395/Domain: protein kinase homology <kin> F;138-146/Region: protein kinase ATP-binding motif F;165/Active site: Lys #status predicted</kin></deb>                                                                                                                                                                 |
|---------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Db   1761 VGSLDHAHIVRLLGLCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLNWGVQIAKGM 820   834 SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEXHADGGKVPIKWAALES 893 | Db 881   HFGKTHOSDWSYGVTWELMTFGAEPYAGLELEIPDLEKGERLAQPQICTIDVTM 940  Qy 954   IMVKCWMIDSECRPRELEVEESRWARDPQREVIOLDGASPLDSTFYRSLLEDDD 1013              | QY 1014 MGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHRHRSSSTRSGGGDLTLGLEPSEE 1068  Db 998 LQEAELEPEL | Qy 1069EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHD 1105                                                                                                                                         | OY 1106 PSPLORYSEDPTVPLPSETDGYVAPLTCSPQPEYUNQPDV 1145                            | OY 1146 RPQPPSPREGPLPAARPAGATLERAKTLSP-GKNGVVKDVFAF 1187  DD 1136 LLTPVTPLSPPGLEEEDGNGYVMPDTHLRGASSSREGTLSSVGLSSVLGTEEEDED 1191 | Oy 1188 GGAVENPEYLTPQGGAAPQPHPP 1210  DD 1192EEYEYMNRKRRGSP-PRPP 1209 | RESULT 11  TVFVLV protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase C;Species: avian leukosis virus, ALV C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999 C;Accession: B00643; A00643 R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines | and<br>so<br>so<br>so |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Query Match         25.9%; Score 1766.5; DB 1; Length 698;           Best Local Similarity 52.2%; Pred. No. 2.4e-65;         Acceal Similarity 52.2%; Pred. No. 2.4e-65;           Matches 374; Conservative 80; Mismatches 137; Indels 125; Gaps 18;           Qy         578 GPEADQCVACAHYKDPPFCVARCESGVKPDLSYMPIWKFPDEGGACQPCPINCTHSCVDL 637           Db         60 GPDHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP 116           Qy         638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQOKIRKYTMBRLQFTEL 696           Cy         638 LDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQOKIRKYTMBRLQFTEL 696 |

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 C;Superfanily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific F;135-40/Domain: protein kinase homology «KIN» F;143-151/Region: protein kinase ATP-binding motif F;170/Active site: Lys #status predicted
 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
 1120 LPSET--DGYVAPLICSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1177
 ----GGAVENPEYLTPQGGAAPQPHPPPAFSPAFD 1218
 ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF 1004
 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1064
 16;
 765
 CMOIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP 885
 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP 945
 --VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLAKTVFE 574
 protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Accession: S35.45

R;Vennstroem, B.

B;Vennstroem, B.

B;Vennstroem, B.

B;Neference number: S35.743

B;Reference number: S35.743
 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
 EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
 418 YRTLMEBEDMEDIVDADEYLVPHQGFF------NSPST-----
 Gaps
25.0%; Score 1703; DB 1; Length 604; 52.2%; Pred. No. 8.2e-63; ive 76; Mismatches 128; Indels 126;
 1219 NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1248
 SSPYWIQSGNHQ-----INLDNPDX
 NGVVKDVFAF-----
 al Similarity 52.2
360; Conservative
 1178
 587
 986
 298
 1005
 Query Match
 29
 904
 994
 178
 826
 238
 450
 A; Gene: erbB
 C, Genetics:
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C;Accession: A00640; A38021
R;Livneh, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.
Call 40, 599-607, 1985
A;Title: The Drosophila EGF receptor gene homolog: conservation of both hormone bindi
A;Reference number: A00640; MUID:85124611; PMID:2982499
 human epidermal growth factor
 1110
 15;
 996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1055
 637
 969
 113
 756
 173
 918
 233
 876
 293
 936
 353
 995
 413
 481
 57
 epidermal growth factor receptor - fruit fly (Drosophila melanogaster)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Drosophila melanogaster
C;bate: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999
 817 LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE
 937 KGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLG
 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ
 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
 GP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP
 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
 VEPLTPSGAMPNQAQMR1LKETELRKVKVLGSGAFGTVYKG1W1PDGENVK1PVA1KVLR
 ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
 YHADGGKVPI KWMALESI LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGI PAREI PDLLE
 1111 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER
 Gaps
 A;Molecule type: DNA
A;Residues: 'A' 832-866,'V',868-943,'OTPSLVK' <WAD>
A;Cross-references: EMBL:X02293; NID:g7922; PIDN:CAA26157.1; PID:g929565
 92;
 Length 544;
 Indels
 ά
 A Molecule type: DNA
A,Residues: 1-1330 <LLIV>
A,Cross-references: EMBL:KO3054
R;Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth,
Nature 314, 178-180, 1985
A;Title: A Drosophila genomic sequence with homology to hu
A;Reference number: A38021; MUID:85137938; PMID:2983232
A;Accession: A38021
Query Match 24.2%; Score 1647; DB 2; Best Local Similarity 54.9%; Pred. No. 1.4e-60; Matches 345; Conservative 70; Mismatches 121;
 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
 LPIDSRYQN-----SHSTAVDNPEYL 544
 A; Accession: A00640
 354
 1170
 524
 28
 697
 757
 174
 877
 294
 455
 482
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| Deen identified.   Qy   669 VVPGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNOAQMRILKETELRKVKV 725 | 1ent) #status pr atus predicted  bb 936 LAARNVLVKLSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRFFTHO  #status predict  OY 903 SDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLDQPPICTIDVYMIMVKCWMID  Dh 903 SDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLDQPPICTIDVYMIMVKCWMID  Dh 903 SDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLDQPPICTIDVYMIMVKCWMID | 39; Qy 963<br>P 134 Db 1052                                                                                               | QY 1018 VDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSSTRSGGGDLTLGLEPSEEEAP 1071       | QY                                                             | QY                                                                 |                                                                     | 424<br>366                                                  | 483<br>426                                                       | 504                       | 504 | VGEGIA 510  C;Superfamily: epidermal growth factor receptor; protein kinase homology  C;Keywords: ATP; phosphotransferase  F;135-40/Domain: protein kinase homology <kin> F;135-15/Perdon: protein kinase homology <kin> F;135-15/Perdon: protein kinase homology <kin></kin></kin></kin> | 562                                                     | 608 Matches 37714 OY 57                            | VVLG 668  OY 638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQCKTRKYTWRRLLQETEL 696  'PTIC 755  Db 58 GLEGCPNGSKTPSIAAGVVGGLLCLVVVCGLGILYLRRR-HIVRKYTRRLLQETEL 113 |
|--------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------|------------------------------------------------------------------|---------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------|----------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| /e not<br>use hom<br>sin; ph                                                               | 700/Binding site: carbohydrate (Asn) (Thr) (covalent) (by protein kinase C s predicted (Tyr) (covalent) (by autophosphoryla (Tyr) (covalent) (by autophosphoryla 24; Score 1645.5; DB 1; Length 1330 34; Pred. No. 3.9e-60;                                                                                                        | <pre>// Conservative 181; Mismate VQGYVLIAHNQVRQVPLQELRIVRGTQLF:                     ITNVIVIGLDLIPCTLSYRLQIIRGRTLF?</pre> | 135 GGLRELQERSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKFIGITELNRSRACHP :   :   : | 195 CSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDC | 253 LACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCUTACPYNYLSTDVGSCT : | 313 LVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFG  1 | 373 SLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAMPDSLPDLSV :: | 425 FONLOVIRGRILHNGAY-SLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD | 484 OLFRNPHQALLHTANRPEDEC | 505 | ARYA                                                                                                                                                                                                                                                                                      | 511CHOLCARGHCWGPGFTQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLP | 563 CHPECQPONGSVTCFGPEADQCVACAHYKDPFCVARCPSGVK-PDL | 609 SYMPIWKEPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLG                                                                                                 |

Search completed: July 22, 2003, 09:08:35 Job time : 30.9062 secs